



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 174903

TO: Manjunath N Rao
Location: rem/3B81/3C70
Art Unit: 1652
Tuesday, January 03, 2006
Case Serial Number: 09/990874

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

mg

174903

STIC-Biotech/ChemLib

From: Rao, Manjunath N.
Sent: Thursday, December 22, 2005 10:59 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request for 09990874

From: Manjunath N. Rao
Art Unit 1652, Room 3B81
Mail Box in Room 3C70
Phone: 272-0939

RECEIVED
DEC 22 AM
STIC

Date: 12-22-05

Please search the following as soon as possible for application with serial number

09/990,874

1. **SEQ ID NO: 55** against all commercial nucleic acid databases, issued patents/published applications database and pending application database.

Please provide a print of all results

If you have any questions please call me at the above phone number.

Thanks

12/22/2005

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus pon model

Run on: December 30, 2005, 00:04:36 ; Search time 3238 Seconds
(without alignments)
3335.471 Million cell updates/sec

Title: US-09-990-874B-55

Perfect score: 1046

Sequence: 1 QTIQPGTGYDGYFYGYWMD.....YQIVAVEGYFSGSASITVS 190

Scoring table:

BLOSUM62
Ygapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlp
-Q=/cgn2_1/USFTO.spool_p/US09990874/runat_29122005_095048_5081/app_query.fasta_1.327
-DB=GenEmbl -QFMT=fastp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09990874 @CGN 1 1 7415 @runat_29122005_095048_5081 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.in.*

3: gb.env.*

4: gb.cm.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 974 | 93.1 | 596 | 6 AX382226 | AX382226 Sequence |
| 2 | 974 | 93.1 | 596 | 6 AX797706 | AX797706 Sequence |
| 3 | 962 | 92.0 | 786 | 15 TRU24191 | U24191 Trichoderma |

| | | | | | |
|----|-------|------|--------|---------------|--------------------|
| 4 | 948 | 90.6 | 573 | 6 AR031735 | AR031735 Sequence |
| 5 | 946 | 90.4 | 1015 | 6 AR055687 | AR055687 Sequence |
| 6 | 946 | 90.4 | 1020 | 15 TRXNIGNA | X69573 T.reesei xy |
| 7 | 946 | 90.4 | 1075 | 15 S67387 | S67387 xln2=endoxy |
| 8 | 870 | 83.2 | 672 | 15 AY320048 | AY320048 Trichoder |
| 9 | 841 | 80.4 | 786 | 15 AY370020 | AY370020 Trichoder |
| 10 | 840 | 80.3 | 841 | 15 AY156910 | AY156910 Trichoder |
| 11 | 834 | 79.7 | 928 | 15 TV1012718 | AJ012718 Trichoder |
| 12 | 723 | 69.1 | 2208 | 15 CENXB2 | D49851 Chaetomium |
| 13 | 700 | 66.9 | 154038 | 15 NC88G12 | BX294027 Neurospor |
| 14 | 687 | 65.7 | 1281 | 6 AR149835 | AR149835 Sequence |
| 15 | 687 | 65.7 | 1281 | 6 CQ847410 | CQ847410 Sequence |
| 16 | 687 | 65.7 | 1281 | 6 AR410556 | AR410556 Sequence |
| 17 | 687 | 65.7 | 1281 | 15 CTH508931 | AJ508931 Chaetomiu |
| 18 | 680.5 | 65.1 | 863 | 15 AY366479 | AY366479 Chaetomiu |
| 19 | 667.5 | 63.8 | 949 | 15 AJ863566 | AJ863566 Gibberell |
| 20 | 658.5 | 63.0 | 687 | 15 AY575961 | AY575961 Gibberell |
| 21 | 656.5 | 62.8 | 1623 | 15 AP814BYL | Z68891 A.pisi endo |
| 22 | 654 | 62.5 | 1409 | 15 ANIDXYLA | Z49892 Aspergillus |
| 23 | 649 | 62.0 | 1921 | 15 AY144350 | AY144350 Magnaport |
| 24 | 645.5 | 61.7 | 89019 | 15 BX842624 | BX842624 Neurospor |
| 25 | 644 | 61.6 | 2102 | 15 AB044941 | AB044941 Aspergill |
| 26 | 643.5 | 61.5 | 588 | 6 AX244978 | AX244978 Sequence |
| 27 | 643.5 | 61.5 | 583 | 6 AR044575 | AR044575 Sequence |
| 28 | 643.5 | 61.5 | 983 | 6 AR157660 | AR157660 Sequence |
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| 32 | 641.5 | 61.3 | 2445 | 1 AB063255 | AB063255 Pseudomon |
| 33 | 640.5 | 61.2 | 851 | 6 A62443 | A62443 Sequence 5 |
| 34 | 639 | 61.1 | 1362 | 15 ANIDXYLB | U01242 Thermomonos |
| 35 | 638.5 | 61.0 | 2196 | 1 U01242 | U01242 Thermomonos |
| 36 | 638.5 | 61.0 | 3204 | 1 AY795559 | AY795559 Thermobif |
| 37 | 638.5 | 61.0 | 110000 | 1 CP000088_14 | Continuation (15 o |
| 38 | 635.5 | 60.8 | 1889 | 15 ASNXNBE | D38070 Aspergillus |
| 39 | 635 | 60.7 | 1174 | 6 AR149836 | AR149836 Sequence |
| 40 | 635 | 60.7 | 1174 | 6 CQ847412 | CQ847412 Sequence |
| 41 | 635 | 60.7 | 1174 | 6 AR410557 | AR410557 Sequence |
| 42 | 635 | 60.7 | 1174 | 15 CTH508932 | AJ508932 Chaetomiu |
| 43 | 633.5 | 60.6 | 695 | 15 CNS01CPS | AL115832 Botrytis |
| 44 | 633 | 60.5 | 1204 | 15 AF301904 | AF301904 Phaneroch |
| 45 | 633 | 60.5 | 1204 | 15 AF301905 | AF301905 Phaneroch |

ALIGNMENTS

| | | | | | | | |
|---------------------------------|------------|-------------|------------------------------------|--------|-----|--------|-----------------|
| RESULT 1 | AX382226 | AX382226 | Sequence 39 from Patent WO0192487. | 596 bp | DNA | linear | PAT 18-MAR-2002 |
| LOCUS | AX382226 | AX382226 | Sequence 39 from Patent WO0192487. | | | | |
| DEFINITION | AX382226 | AX382226 | Sequence 39 from Patent WO0192487. | | | | |
| ACCESSION | AX382226 | AX382226 | Sequence 39 from Patent WO0192487. | | | | |
| VERSION | AX382226.1 | GI:19577009 | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| FEATURES | | | | | | | |
| source | | | | | | | |
| 1..596 | | | | | | | |
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| /db_xref="taxon:32630" | | | | | | | |
| /note="TrX" | | | | | | | |

ORIGIN

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|-------------------|----------|----------|-----|--|--|
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| Pred. No.: | 1.17e-78 | Length: | 596 | | |
| Score: | 974.00 | Matches: | 179 | | |

Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AX382226 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
 DB 23 CAAACAATACACACAGGACCGGTTACAAACACCGGTTACTTTTACAGCTATTGGAACGAT 82

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
 DB 83 GGCCATGGTGGTGTACTTATACAAACCGGCCCGGAGGCCAAATTTAGCGTCAATTTGGTCT 142

QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
 DB 143 AACTCCGGAAACTTCGTAGGTGGAAAGGTTGGCAACCGCGGACCAAAAAATAAGGTGATC 202

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSer 80
 DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGGTCT 262

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAAACCCACTGATTGTAATATTCATTTGCGAAATTTCCGTACTACATCCGAGTACC 322

QY 101 GlyAlaThrLysHisGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 DB 323 GGCGCCACAAAATTAGCGCAAGTCACTAGTATGATGATGATGATGATGATGATGATGATGAT 382

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
 DB 383 CAACGCGTTAATCAGCCATCGATCATTTGGAACCGGCCACCTTTTATCAGTACTGGAGTGT 442

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
 DB 443 AGAGTATATCATCGAGCTCCGTTCCGTTTAACTCGAATCACTTTAATGCATGGCA 502

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 503 CAGCAAGGTTTAACTTACCTTAGGTACAAATGATGATGATGATGATGATGATGATGATGAT 562

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 563 TCGAGTGGTTCCTCGCTAGTATTACAGTGAGC 592

RESULT 2
 AX797706 AX797706 596 bp DNA linear PAT 04-OCT-2003
 LOCUS
 DEFINITION Sequence 39 from Patent WO03046169.
 ACCESSION AX797706
 VERSION AX797706.1 GI:37518114

KEYWORDS
 SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
 ORGANISM Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
 1 Sung, W. L.
 Xylanases with enhanced thermophilicity and alkalophilicity
 Patent: WO 03046169-A 39 05-JUN-2003;
 National Research Council of Canada (CA)
 Location/Qualifiers
 1. .596
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FEATURES
 source
 synthesized Trx sequence produced using synthetic
 oligonucleotide (SEQ ID Nos.21-38) as depicted in Figure
 2"

ORIGIN

Alignment Scores:
 Pred. No.: 1,17e-78 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AX797706 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20

DB 23 CAAACAATACACACAGGACCGGTTACAAACACCGGTTACTTTTACAGCTATTGGAACGAT 82

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40

DB 83 GGCCATGGTGGTGTACTTATACAAACCGGCCCGGAGGCCAAATTTAGCGTCAATTTGGTCT 142

QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60

DB 143 AACTCCGGAAACTTCGTAGGTGGAAAGGTTGGCAACCGCGGACCAAAAAATAAGGTGATC 202

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSer 80

DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGGTCT 262

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100

DB 263 AGAAACCCACTGATTGTAATATTCATTTGCGAAATTTCCGTACTACATCCGAGTACC 322

QY 101 GlyAlaThrLysHisGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120

DB 323 GGCGCCACAAAATTAGCGCAAGTCACTAGTATGATGATGATGATGATGATGATGATGATGAT 382

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140

DB 383 CAACGCGTTAATCAGCCATCGATCATTTGGAACCGGCCACCTTTTATCAGTACTGGAGTGT 442

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160

DB 443 AGAGTATATCATCGAGCTCCGTTCCGTTTAACTCGAATCACTTTAATGCATGGCA 502

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180

DB 503 CAGCAAGGTTTAACTTACCTTAGGTACAAATGATGATGATGATGATGATGATGATGATGAT 562

QY 181 SerSerGlySerAlaSerIleThrValSer 190

DB 563 TCGAGTGGTTCCTCGCTAGTATTACAGTGAGC 592

RESULT 3
 TRU24191 786 bp mRNA linear PLN 25-MAR-1997
 LOCUS
 DEFINITION Trichoderma reesei beta-xylanase (XYN2) mRNA, complete cds.
 ACCESSION U24191
 VERSION U24191.1 GI:780815

KEYWORDS
 SOURCE Hypocrea jecorina
 ORGANISM Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
 1 (bases 1 to 786)
 la Grange, D.C., Pretorius, I.S. and van Zyl, W.H.
 Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
 Saccharomyces cerevisiae
 Appl. Environ. Microbiol. 62 (3), 1036-1044 (1996)

REFERENCE
 2 (bases 1 to 786)
 van Zyl, W.
 Direct Submission
 Submitted (06-APR-1995) Willem H. van Zyl, University of
 Stellenbosch, Microbiology, Victoria street, Stellenbosch, 7600,

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FEATURES             South Africa
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CDS                  105. .776
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mat_peptide          204. .773
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Query Match:        91.97%       Indels:     0
DB:                 15           Gaps:       0

US-09-990-874B-55 (1-190) x TRU24191 (1-786)
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QY  21  GlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer  40
DB  264 GGCACGCGCGGTGACGTACACCAATGGTCCCGCGCGGAGTCTCCGTCAACTGGTCC  323
QY  41  AsnSerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrLysAsnLysValIle  60
DB  324 AACTCGGGCAACTTTGTTCGGCGGCAAGGGATGGCAGCCCGGACCAAGAACAGGTGATC  383
QY  61  AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer  80
DB  384 AACTTCGGGCGAGCTACACCCGACCGGACAGCTACTCTCCGTGTAGCGTGGTCC  443
QY  81  ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr  100
DB  444 CGCAACCCCTGATCGAGTACTACATCGTCGGGAATTTGGCACCTACACCCGTCACG  503
QY  101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr  120
DB  504 GGGCGCCACCAAGCTGGGCGAGGTCACTCCGACGGCAGCGCTACGACATTTACCGCAGC  563
QY  121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal  140
DB  564 CACGGGTCAACGACCGCTCATCATCGGCACCGCCACCTTTTACAGTACTGGTCCGTC  623
QY  141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla  160
DB  624 CGCGCAACCAACCGCTCGAGCGGTCCGTCAACACGCGGACCAACCACTTCAACGCGTGGCT  683
QY  161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe  180
DB  684 CAGCAAGGCGCTGACGCTCGGACGATGATACAGATTGTCGCGTGGAGGGTACTTTT  743
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QY  181 SerSerGlySerAlaSerIleThrValSer  190
DB  744 AGCTCTGGCTCTGCTTCCATCACCGTCAGC  773

RESULT 4
AR031735 LOCUS
DEFINITION Sequence 18 from patent US 5866408.
ACCESSION AR031735
VERSION AR031735.1 GI:5946024
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 573)
AUTHORS Sung W.L., Yaguchi M. and Iehikawa K.
TITLE Modification of xylanase to improve thermophilicity, alkophilicity
and thermostability
JOURNAL Patent: US 5866408-A 18 02-FEB-1999;
FEATURES Location/Qualifiers
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Best Local Similarity: 92.06%    Mismatches: 9
Query Match:        90.63%       Indels:     0
DB:                 6           Gaps:       0

US-09-990-874B-55 (1-190) x AR031735 (1-573)
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DB  3  AGCATAGGACCAAGAAACCGGTTTCAACACCGTTACTTTTACAGCTATTTCGAACGATGCG  62
QY  22  HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn  41
DB  63 CATGGTGGTGTATACCTATACAAACGGGCGCGGAGGCAATTTAGCGCTCAATTTGGTCTAAC  122
QY  42  SerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIleAsn  61
DB  123 TCCGGAAACTTCGTAGTGGAAAGGTGGCAACCGGACCAAAATAAGGTGATCAAC  182
QY  62  PheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg  81
DB  183 TTCTCTGGATCTTATAATCGAATGGGAATTCATCTTAAGCGTCTATGCTGTCTAGA  242
QY  82  AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGly  101
DB  243 AACCCACTGATTGAATATTACATTGTCGAAATTTTCGGTACCTACCAATCCGAGTACCGGC  302
QY  102 AlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGln  121
DB  303 GCCACAAATTAGGCGAAGTCACTAGTGGATCGGTATGATATATATCTACCGTACCCAA  362
QY  122 ArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArg  141
DB  363 CGGTTAATCAGCCATCGATCATTTGGAACCGGCACCTTTTATCAGTACTGGAGTGTAGA  422
QY  142 ArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArg  161
DB  423 CGTACCGCATCGGAGCTCCGGTTCGGTTAATACGCAATCAGTATGATGATGATGATGATGAT  482
QY  162 GlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer  181
DB  483 CAGGGGTAAACCCCTAGGTACATGGAATATCAATGATGCGGTGGAGGCTACTTCTCG  542
QY  182 SerGlySerAlaSerIleThrValSer  190
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Db      543 AGTGGTTCGGCTAGTATTACAGTGAGC 569
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RESULT 5
AR055687 LOCUS 1015 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5837515.
ACCESSION AR055687
VERSION AR055687.1 GI:5981264
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1015)
  Suomen,P., Nevalainen,H., Saarelainen,R., Paloheimo,M. and
  Fagerstrom,R.
  Enzyme preparations and methods for their production
  Patent: US 5837515-A 1 17-NOV-1998;
  Location/Qualifiers
    source 1..1015
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ORIGIN
Alignment Scores:
Pred. No.: 7,06e-76 Length: 1015
Score: 946.00 Matches: 179
Percent Similarity: 80.97% Conservative: 4
Best Local Similarity: 79.20% Mismatches: 7
Query Match: 90.44% Indels: 36
DB: 6 Gaps: 1

US-09-990-874B-55 (1-190) x AR055687 (1-1015)

Qy      1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTripanNap 20
Db      275 CAGACGATTTCAGCCGCGCAGCGGCTACAAACACGGCTACTTCTACTCGTACTGGAACGAT 334
|||||
Qy      21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTripanSer 40
Db      335 GGCCACGCGCGGTGACGTACACCAATGGTCCCGCGCGGCGAGTTCTCCGTCACTGGTCC 394
|||||
Qy      41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLys----- 58
Db      395 AACTCGGCAACTTGTTCGGCGGCAAGGATGGCAGCCCGGACCAAGAACAGTAAGAC 454
|||||
Qy      58 ----- 58
Db      455 TACCTACTCTTACCCCTTTGACCAACACAGCAACACATACAAACACATGTGACTACC 514
Qy      59 -----ValIleAsnPheSerGly 64
Db      515 AATCATGGAATCGGATCTAACACAGCTGTGTTTAAAAAAAAGGGTCACTCACTTCGCGGA 574
|||||
Qy      65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu 84
Db      575 AGCTACAACCCCAACGCGCAACAGTACTCTCCGCTAGCGGTGTCGCGCAACCCCTG 634
|||||
Qy      85 IleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLys 104
Db      635 ATCCAGTACTACATCGTCGAGAACCTTTGGCACCCTACAAACCCGCTCCACGGGGCCACCAAG 694
|||||
Qy      105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
Db      695 CTGGCGAGAGTCACTCCGCGGCGAGCTCTACGACATTTACCCGACCGCGCGCTCAAC 754
|||||
Qy      125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgArgAsnArg 144
Db      755 CAGCCGTCCATCATCGGCACCGCCACCTTTTACCAAGTACTGTGCTCGCGCGCAACAC 814
|||||
Qy      145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTripanNapGlnGlyLeu 164
Db      815 CGCTCAGCGGCTCGTCAACACGCGGAACCACTTCAACGCGGTGGGCTCAGCAAGGCGCTG 874
|||||
Qy      165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
Db      875 ACGTCTCGGACGATGGATTACAGATTGTTGCCGTGGAGGGTACTTATAGCTCTGGCTCT 934
|||||
Qy      185 AlaSerIleThrValSer 190
Db      935 GCTTCCATCACCGTCAGC 952
|||||
RESULT 6
TRXYNIGNA
LOCUS 1020 bp DNA linear PLN 16-NOV-1993
DEFINITION T.reesei xynl gene, complete CDS.
ACCESSION X69573.1 GI:396563
VERSION X69573.1
KEYWORDS xyl gene; xylanase.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
REFERENCE
  1 (bases 1 to 1020)
  Hypocreomycetidae; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Eukaryota; Hypocreales; Hypocreaceae; Hypocreaceae; Hypocrea.
  Torronen,A., Mach,R.L., Messner,R., Gonzalez,R., Kalkkinen,N.,
  Harkki,A. and Kubicek,C.P.
  The two major xylanases from Trichoderma reesei: characterization
  of both enzymes and genes
  Biotechnology (N.Y.) 10 (11), 1461-1465 (1992)
  1369024
  Location/Qualifiers
    source 1..1020
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    /db_xref="taxon:51453"
    199...975
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    576...>975
    /gene="xynl"
    /number=2

ORIGIN
Alignment Scores:
Pred. No.: 7,1e-76 Length: 1020
Score: 946.00 Matches: 179
Percent Similarity: 80.97% Conservative: 4
Best Local Similarity: 79.20% Mismatches: 7
Query Match: 90.44% Indels: 36
DB: 15 Gaps: 1

US-09-990-874B-55 (1-190) x TRXYNIGNA (1-1020)

Qy      1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTripanNap 20
Db      295 CAGACGATTTCAGCCGCGCAGCGGCTACAAACACGGCTACTTCTACTCGTACTGGAACGAT 354
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Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 355 GGCCACGGCGGCGTACCAATGATGTCGCGGGGCGAGTCTCGGTCAACTGGTCC 414
Qy 41 AsnSerGlyAsnPheValGlyGlyysGlyTrpGlnProGlyThrLysAsnLys----- 58
Db 415 AACTCGGGCAACTTTGTGCGGGCAAGGATGGCAGCGCGCCGCAACCAAGAAACAGTAAGAC 474
Qy 58 ----- 58
Db 475 TACCTACCTTACCCCTTTGACCAACACAGCACACACAAATACACACATGTCAGTACC 534
Qy 59 -----ValIleAsnPheSerGly 64
Db 535 AATCATGGAATCGGATCTAACAGCTGTGTTTCAAAAAAGGGTCATCAACTTCTCGGGC 594
Qy 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeu 84
Db 595 AGCTACAACCCCAACGGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTG 654
Qy 85 IleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLys 104
Db 655 ATCGAGTACTACATCTGTCGAGAACTTTGGCACCTTACCAACCGCTCCAGCGGCCCAACAG 714
Qy 105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
Db 715 CTGGCGAGGTCACTTCGAGCGGCGAGGTCTACGACATTTACCGCACGCGCGGTCAAC 774
Qy 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArg 144
Db 775 CAGCGGTCCATCATCGGCACCGCCACCTTTTACCAGTACTTGGTCCGTCGCGCGCAACAC 834
Qy 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeu 164
Db 835 CGTCGAGCGGTCCGTCACACCGCGCAACCACTTCAACCGGTGGGTCTCAGCAAGGCGTG 894
Qy 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
Db 895 ACCTCGGAGCATGGATTACAGATTGTTGCGGTGGAGGGTTACTTTAGCTCTGGTCT 954
Qy 185 AlaSerIleThrValSer 190
Db 955 GCTTCCATCACCGTCAGC 972

RESULT 7
S67387
LOCUS
DEFINITION
xln2-endoxylanase II [Trichoderma reesei, ALKO2721, VTT-D-79125,
Genomic, 1075 nt].
ACCESSION
S67387
VERSION
S67387.1 GI:455906
KEYWORDS
Hypocrea jecorina
SOURCE
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE
1 (bases 1 to 1075)
Saarelainen, R., Paloheimo, M., Pajestrom, R., Suominen, P. L. and
Nevalainen, K. M.
Cloning, sequencing and enhanced expression of the Trichoderma
reesei endoxylanase II (pi 9) gene xln2
Mol. Gen. Genet. 241 (5-6), 497-503 (1993)
JOURNAL
8264524
PUBMED
GenBank staff at the National Library of Medicine created this
entry [NCBI Gibbsq 140980] from the original journal article.
REMARK
Location/Qualifiers
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176..955
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join(176..447,556..955)
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IGTATFYIWSVRNRHRSRGSVNTAHNFNAQAQGLTLGTMDIQTIVAVEGFSFGSA
SITVS"
ORIGIN
Alignment Scores: 7,53e-76 Length: 1075
Pred. No.: 946.00 Matches: 179
Score: 946.00 Conservative: 4
Percent Similarity: 80.97% Mismatches: 7
Best Local Similarity: 79.20% Indels: 36
Query Match: 90.44% Gaps: 1
DB: 15
US-09-990-874B-55 (1-190) x S67387 (1-1075)
Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db 275 CACACGNTTCAGCCCGGCGGCTACACACACGGCTACTTCTACTCGTACTGGACGAT 334
Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 335 GGCCACGGCGGCTGACGTACCAATGGTCCGCGGCGGAGTCTCCGTCAACTGGTCC 394
Qy 41 AsnSerGlyAsnPheValGlyGlyysGlyTrpGlnProGlyThrLysAsnLys----- 58
Db 395 AACTCGGGCAACTTTGTGCGGGCAAGGGATGGAGCCCGGGACCAAGAAACAGTAAGAC 454
Qy 58 -----ValIleAsnPheSerGly 64
Db 455 TACCTACTTACCCCTTTGACCAACACAGCACACACAAATACACACATGTCAGTACC 514
Qy 59 -----ValIleAsnPheSerGly 64
Db 515 AATCATGGAATCGGATCTAACAGCTGTGTTTAAAAAAGGGTCATCAACTTCTCGGA 574
Qy 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeu 84
Db 575 AGCTACAACCCCAACGGCAACAGCTACCTCTCGGTGTACGGTGGTCCCGCAACCCCTG 634
Qy 85 IleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLys 104
Db 635 ATCGAGTACTACATCTCGAGAACTTTGGCACCTACACCCGCTCCAGCGGCGCCACCAAG 694
Qy 105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
Db 695 CTGGCGGAGGTCACTCCGAGCGGCGAGCTACGACATTTACCGCACGCGAGCGGTCAAC 754
Qy 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArg 144
Db 755 CAGCGGTCCATCATCGGCACCGCCACTTTTACCAGTACTGGTCCGTCGCCGCCCAACAC 814
Qy 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeu 164
Db 815 CGCTCAGCGGTCTCCGTCAACACGGCGAACCATTTCACCGGTGGGTCTCAGCAAGGCTG 874
Qy 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
Db 875 AGGCTCGGGAGGATGGATTACAGATTGTTGCGGTGGAGGGTTACTTTAGCTCTGGTCT 934
Qy 185 AlaSerIleThrValSer 190
Db 935 GCTTCCATCACCGTCAGC 952
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RESULT 8
AY320048          672 bp  mRNA  linear  PLN 14-JUL-2003
LOCUS
DEFINITION
Trichoderma viride strain YNUCC0183 endo-1,4-beta-xylanase mRNA,
complete cds.
ACCESSION
AY320048
VERSION
AY320048.1  GI:32481056
KEYWORDS
Trichoderma viride
SOURCE
Trichoderma viride
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma; Trichoderma viride species complex.
REFERENCE
1 (bases 1 to 672)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Zhou, J.G., Yang, Y.H., Liu, W.J. and
Yang, Z.W.
TITLE
Cloning and characterization of endo-1,4-beta-xylanase from
Trichoderma viride YNUCC0183
JOURNAL
2 (bases 1 to 672)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Zhou, J.G., Yang, Y.H., Liu, W.J. and
Yang, Z.W.
TITLE
Direct Submission
JOURNAL
Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology &
Fermentation Technology of Yunnan, School of Life Science, Yunnan
University, 2 North Road, Green Lake, Kunming, Yunnan 650091, China
FEATURES
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CDS
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NINVS"
ORIGIN
Alignment Scores: 3.1e-69 Length: 672
Pred. No.: 870.00 Matches: 156
Score: 89.47% Conservative: 14
Percent Similarity: 82.11% Mismatches: 20
Best Local Similarity: 83.17% Indels: 0
Query Match: 15 Gaps: 0
DB:
US-09-990-874B-55 (1-190) x AY320048 (1-672)
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
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Db 100 CAGACGATTGGCCCGGACATGGCTTCAACACGGCTACTACTACTCTGACTCGAAGCAT 159
|||||
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
|||||
Db 160 GGCCATTCCGGCGTGACATACCAACCGGTGCTGGCGCTCATTCAGCGTCAACTGGCA 219
|||||
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyTyrGlnProGlyThrLysAsnLysValIle 60
|||||
Db 220 AACTCGGGCAACTTTGTTCGAGGCAAGGGATGGAACCCCGGCACTCCAGGGTCATC 279
|||||
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
|||||
Db 280 AACTTCTCTGGCAGCTACACCCCAACGGCATAGTACCTCTCAGTCTATGGCTGTGCA 339
|||||
QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
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Db 340 AAGAACCTCTCATCGAGTACTACATCGTTGAGAACTTTGGAACTTACACCATCGACC 399
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
|||||
Db 400 GGCACACCAAGCTGGCGAGGTGACCTCTGACGGCAGCGTCTACGACATCTACCGCAGC 459
|||||
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
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Db 460 CAGCGAGTCAACGAGCTTCCATCATCGGAACCGCCACCTTTTACCAGTACTGCTCTGTC 519
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QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
|||||
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Db 580 AACCTGGGCTTGACCTGGGACCTTGGACTACGACATCATTCGCGTGGAGGCTACTTT 639
|||||
QY 181 SerSerGlySerAlaSerIleThrValSer 190
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Db 640 AGCTCTGGTAAGCCCAACATTAAACGTTAGC 669
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RESULT 9
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LOCUS
DEFINITION
Trichoderma viride strain YNUCC0183 endo-1,4-beta-xylanase (XYL1)
gene, complete cds.
ACCESSION
AY370020
VERSION
AY370020.1  GI:34420135
KEYWORDS
Trichoderma viride
SOURCE
Trichoderma viride
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma; Trichoderma viride species complex.
REFERENCE
1 (bases 1 to 786)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Liu, S.Q., Zhou, J.G. and Liu, W.J.
TITLE
Cloning and characterization of endo-1,4-beta-xylanase from
Trichoderma viride YNUCC0183
JOURNAL
Unpublished
2 (bases 1 to 786)
AUTHORS
Li, W.P., Zhang, Q., Liao, C.L., Liu, S.Q., Zhou, J.G. and Liu, W.J.
TITLE
Direct Submission
JOURNAL
Submitted (18-AUG-2003) Key Laboratory of Industrial Microbiology &
Fermentation Technology of Yunnan, School of Life Science, Yunnan
University, 2 North Road, Green Lake, Kunming, Yunnan 650091, P.R.
China
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NINVS"
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Alignment Scores:

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Pred. No.: 1,51e-66 Length: 786
Score: 841.00 Matches: 156
Percent Similarity: 74.56% Conservative: 14
Best Local Similarity: 68.42% Mismatches: 20
Query Match: 80.40% Indels: 38
DB: 15 Gaps: 1

US-09-990-874B-55 (1-190) x AY370020 (1-786)

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Db 100 CAGACGATTCGGCCCGGCACTGGCTTCAACAACGGCTACTACTCGTACTGGACGAT 159

QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
Db 160 GGCATTCGGCGTGACATACCAACGCGTCTGGCGGCTCATTCAGCGTCACTGGGCA 219

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLys----- 56
Db 220 AACTCGGCAACTTGTTCGGAGGCAAGGATGGAACCCCGGACGAGCTCCAGGTAAAGT 279

QY 56 ----- 56
Db 280 ACTCAAGTGAGGAACACAACTCAGATACCTCAAGACACTGCCACCACTGCCCTGTG 339

QY 57 -----AsnLysValIleAsnPhe 62
Db 340 CCAATTCAGTCGAGAGAGCTAATACCACTCGCTGTGTAATCAAGGTCATCACTTC 399

QY 63 SerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsn 82
Db 400 TCTGGCAGCTACAAACCCCAAGCGCAATAGCTACCTCTCAGTCTATGCTGCTCAAGAAC 459

QY 83 ProLeuIleGluTyrThrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAla 102
Db 460 CCTCTCATCGAGTACTACATCGTTGAGAACTTTGGAACTTACCAACCCATCGACGGCACC 519

QY 103 ThrLysHisGlyGluValThrSerAspGlySerValTyrAspLysCysArgThrGlnArg 122
Db 520 ACCAGCTGGCGAGGAGTACTCTGACGGCAGGCTTACGACATCTACCGACGACGCGA 579

QY 123 ValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgArg 142
Db 580 GTCAACACGCTTCCATCATCGAGACCGCCACCTTTTACAGTACTGCTGTGCGCGCG 639

QY 143 AsnArgArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGln 162
Db 640 AACACCGCTCCAGCGGCTCGGTACCGTTCGGAACCACTTCAACGCGTGGCGCAACCTG 699

QY 163 GlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSer 182
Db 700 GGTTCACCTCGGAACCTTGGACTACCAATCATTCGCGGAGGCTACTTTAGTCTCT 759

QY 183 GlySerAlaSerIleThrValSer 190
Db 760 GGTACGCCCAACATTAACTGTAGC 783

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RESULT 10

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AY156910 841 bp mRNA linear PLN 11-DEC-2002
LOCUS Trichoderma sp. SY xylanase mRNA, complete cds.
DEFINITION Trichoderma sp. SY
ACCESSION AY156910
VERSION AY156910.1 GI:26514829
KEYWORDS Trichoderma
SOURCE Trichoderma
ORGANISM Trichoderma sp. SY
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma.
REFERENCE 1 (bases 1 to 841)
AUTHORS Min.S.Y., Kim.B.G. and Ahn,J.-H.
TITLE Purification, Characterization, and cDNA Cloning of Xylanase from

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Fungus Trichoderma Strain SY

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Unpublished
REFERENCE 2 (bases 1 to 841)
AUTHORS Min.S.Y., Kim.B.G. and Ahn,J.-H.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-2002) Forest and Environmental Science, Konkuk
University, 1 Hwayang-Dong, Kwangjin-Gu, Seoul 143-701, South Korea
FEATURES
Location/Qualifiers
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VS"

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ORIGIN

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Alignment Scores:
Pred. No.: 2,01e-66 Length: 841
Score: 840.00 Matches: 151
Percent Similarity: 86.84% Conservative: 14
Best Local Similarity: 79.47% Mismatches: 25
Query Match: 80.31% Indels: 0
DB: 15 Gaps: 0

US-09-990-874B-55 (1-190) x AY156910 (1-841)

QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
Db 150 CAGGTCAATTCGGCCCGGCACTGGCTTCAACAACGGCTACTACTCGTACTGGACGAC 209

QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSer 40
Db 210 GGCATTCGGCGTGACATACCAACGCGCTGGCGGCTCTACGCTCACTGGGCCC 269

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
Db 270 AACTCGGCAACTTGTTCGGAGGCAAGGATGGAACCCCGGCGACGACGACCAACCATC 329

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSer 80
Db 330 AACTTCTCGGCGAGCTACAGCCCAACGACCAACAGCTACTCTCTCGTCTACGGCTGCTCC 389

QY 81 ArgAsnProLeuIleGluTyrThrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 390 AAGAACCCGCTCATCGAGTACTACATGTGCGAGAACTTTTGGCACCTTACCAACCGTCCAGC 449

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspLysCysArgThr 120
Db 450 GGGCCCAACCAAGCTGGCGAGGTGACGCTCGACGGCGAGCGCTTACGACATTTACCGCACG 509

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerVal 140
Db 510 CAGCGGCTCAACGACGCTCCATCATCGGCACCGCCACCTTTTACCAAGTACTCGTCCGCTG 569

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAla 160
Db 570 CGCCCGCACCAACCGCTCCCGGCGGCTCGGTCAACGTTGGGCGGCAACCACTTCAATCGCTGCGCC 629

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
Db 630 AATCTCGGCTGACGCTGGGACAGCTGAGTACTACAGATTATTGCGCGTGGAGGATATTTC 689

QY 181 SerSerGlySerAlaSerIleThrValSer 190

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Db      690 AGCTCTGCGAGCGCCCAACATTAACTGTCAGC 719

RESULT 11
LOCUS   TVI012718      928 bp      mRNA      linear      PLN 15-APR-2005
DEFINITION Trichoderma viride mRNA for endo-1,4-beta-xylanase.
ACCESSION AJ012718
VERSION   A2012718.1 GI:6434132
KEYWORDS  endo-1,4-beta-xylanase.
SOURCE    Trichoderma viride
ORGANISM  Trichoderma viride
          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
          Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
          Trichoderma; Trichoderma viride species complex.
REFERENCE
AUTHORS   Furman-Matarasso, N., Cohen, E. and Avni, A.
TITLE      Mutations in the Active Site of the Ethylene Inducing Xylanase
           Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the
           Elicitation Activity
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 928)
AUTHORS   Avni, A.
TITLE      Direct Submission
JOURNAL   Submitted (10-NOV-1998) Avni A., Plant Sciences, Tel-Aviv
           University, Tel-Aviv University, Tel-Aviv, 69978, ISRAEL
FEATURES
          Location/Qualifiers
            source          1..928
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ORIGIN
Alignment Scores:
Pred. No.:      7,79e-66      Length:      928
Score:          834.00      Matches:     156
Percent Similarity: 89.01%      Conservative: 14
Best Local Similarity: 81.68%      Mismatches:  20
Query Match:    79.73%      Indels:      2
DB:             15      Gaps:         0

US-09-990-874B-55 (1-190) x TVI012718 (1-928)

Qy      1  GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db      162 CAGACGATTGGCCCCGGGACCTGGCTTCAACACCGCTACTACTCTCTCTCTGAGTCTATGCGTGC 221
Qy      21  GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db      222 GGCATTCCGGCGTGACATACACCAACGCTGCGGCTCATTCAGCGTCACTGGGCA 281
Qy      41  AsnSerGlyAsnPheValGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIle 60
Db      282 AACTCGGGCACTTTGTTCGGAGGCAAGGATGGAACCCCTGCGCAGCAGCTCCAGAGTCATC 341
Qy      61  AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80

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Db      342 AACTTCTCTGCGAGCTACAAACCCCAACGGCAACAGCTACCTCTCAGTCTATGCGTGC 401
Qy      81  ArgAsnProLeuIleGlnTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db      402 AAGAACCCCTCATCAGTAGTACTACTTGTGTGAGAACTTTGGAACCTTGAACCTCAACCCATCGACT 461
Qy      101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db      462 GGCACCAACCAAGCTGGGTGAGGTGACCTCTGACGGCAGCGCTCTACGACATCTACCGCAGC 521
Qy      121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db      522 CAGCGAGTCAACAGCGCTTCCATCATCGGAACGGCCACCTTTTACCAGTAGTACTGCTGTC 581
Qy      141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPhe-AsnAlaTrpAl 160
Db      582 CGCGCGCAACCA-CGCTCCAGCGGCTCGGTCCACGGTTGCGAACCACCTTCCAAACGGGTGGCG 640
Qy      160 aArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPh 180
Db      641 CAACCTGGGCTTGACTCTGGGAACCTTGGACTACCACTCATTCGCTGGAGGGGCTACTT 700
Qy      180 eSerSerGlySerAlaSerIleThrValSer 190
Db      701 TAGCTCTGTTAAGCCCAACATTAACTGTCAGC 731

RESULT 12
CEMKB2   2208 bp      DNA      linear      PLN 14-APR-2000
LOCUS    Chaetomium gracile endo-beta1,4-xylanase B (cgxB) gene, complete
DEFINITION
ACCESSION D49851
VERSION   D49851.1 GI:1339859
KEYWORDS  cgxB; endo-beta1,4-xylanase.
SOURCE    Chaetomium gracile
ORGANISM  Chaetomium gracile
          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
          Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
REFERENCE
AUTHORS   Yoshino, S., Oishi, M., Moriyama, R., Kato, M. and Tsukagoshi, N.
TITLE      Two family G xylanase genes from Chaetomium gracile and their
           expression in Aspergillus nidulans
JOURNAL   Curr. Genet. 29 (1), 73-80 (1995)
PUBMED    8595661
REFERENCE  2 (bases 1 to 2208)
AUTHORS   Tsukagoshi, N.
JOURNAL   Unpublished
REFERENCE  3 (bases 1 to 2208)
AUTHORS   Tsukagoshi, N.
TITLE      Direct Submission
JOURNAL   Submitted (25-MAR-1995) Norihiro Tsukagoshi, Nagoya University,
           Faculty of Agriculture, Applied Biological Sciences, Furo-cho,
           Chikusa-ku, Nagoya, Aichi 464-01, Japan
           (E-mail: i45370a@nucc.cc.nagoya-u.ac.jp, Tel:052-789-4086,
           Fax:052-789-4087)
FEATURES
          Location/Qualifiers
            source          1..2208
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intron

exon

ORIGIN

Alignment Scores:
Pred. No.: 2,05e-55 Length: 2208
Score: 723.00 Matches: 130
Percent Similarity: 76.88% Conservative: 23
Best Local Similarity: 65.33% Mismatches: 30
Query Match: 69.12% Indels: 16
DB: 15 Gaps: 1

US-09-990-874B-55 (1-190) x CEMXB2 (1-2208)

Qy 7 ThrGlyTyrHisLeuGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThr 26
Db 898 ACTGGACCAACACCGCTACTACTCTGTTCTGGACTGACGCCAGGCGACGTCAG 957
Qy 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
Db 958 TACACCAACGAGGCTGGCGGCCAGTACAGCGTGGTGGCGACGCGCATTTGGGTC 1017
Qy 47 GlyGlyLysGlyTyrGlnProGlyThrLysAsn----- 57
Db 1018 GCGCGCAAGGCTGGAACCGCGCGAGTGTCTCGTACGCTCTCTATTACTAGACACCGATC 1077
Qy 58 -----LysValIleAsnPheSerGlySerTyrAsnProAsnGly 70
Db 1078 TTTCATGGCTAACGCCCTTTTCAGACCATCACTACACGCCCACTACACCCCAACGCC 1137
Qy 71 AsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeuIleGluTyrIleVal 90
Db 1138 AACTCGTACTTGGCGCTCTACGGCTGACGCGCACCCCGTTGATCGAGTATTATGTTT 1197
Qy 91 GluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSer 110
Db 1198 GAGAACTTTGGCAGCTACAAACCCCTGACGCGCGCCACCCCGCTGGCGCGTGCAGCAC 1257
Qy 111 AspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluGly 130
Db 1258 GACGGGTCTTGTCTACGACATCTACCGCACGCGCGCTCAACCGCGCTCGATCGAGGGT 1317
Qy 131 ThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerSerGlySerVal 150
Db 1318 ACCAGACCTTCTACCAATTTCTGGTGGTGGCGCAGAACAGCGCAGCGCGGCGAGGCTC 1377
Qy 151 AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAsp 170
Db 1378 AACATGCGCCGCCACTTCAACGCGCTGGCGCGCGCGCGCTGCGAGCTGGCGCACCCACG 1437
Qy 171 TyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
Db 1438 TACCAGATTGTCGCCACCGAGGGGCTACTACTCGAGCGGCTCTGCGACCGTCAACGTC 1494

RESULT 13

NCB8G12/c 154038 bp DNA linear PLN 17-APR-2005
LOCUS Neurospora crassa DNA linkage group V BAC contig B8G12.

DEFINITION BX294027

ACCESSION BX294027.1

VERSION GI:28950191

KEYWORDS

SOURCE Neurospora crassa

ORGANISM Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

REFERENCE

AUTHORS

JOURNAL

AUTHORS

TITLE

JOURNAL

1

Schulte,U., Aign,V., Hoheisel,J., Brandt,P., Fartmann,B.,
Holland,R., Nyakatura,G., Mewes,H.W. and Mannhaupt,G.

Unpublished

2 (bases 1 to 154038)

German Neurospora genome project.

Direct Submission

Submitted (11-MAR-2003) MIPS, Institut fuer Bioinformatik,

GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,

Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:

G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute

of Biochemistry, Heinrich-Heine-University, D-40225 Dueseldorf,

E-mail: ulrich-schulte@uni-dueseldorf.de

this contig is an assembly of BAC 7G12 from 1 to: 79514, cosmid

6585 from 79515 to: 119973 and BAC 7L15 from 119974 to:154038; BACS

(strain OR74A) and cosmid clones (library pLORIS76Xh, strain

74-OR-23-1A) are available at the Fungal Genetic Stock Center,

http://www.fgsc.net Sequencing was performed by MWG Biotech AG,

Ebersberg, Germany, http://www.mwgdna.com

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of linkage groups II

and V can be viewed at: http://mips.gsf.de/proj/neurospora.

Location/Qualifiers

1. 154038

/organism="Neurospora crassa"

/mol_type="genomic DNA"

/db_xref="taxon:5141"

/chromosome="2"

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/gene="B8G12.010"

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/gene="B8G12.010"

complement(join(3021..3627,3708..3982))

/gene="B8G12.010"

/note="strong similarity to endo-1, 4-beta-xylanase (EC

3.2.1.8) B precursor, Chaetomium gracile, FIR:S71473

Contains Cellulose-binding domain, fungal type

[CGGQWGSATCCSGSTCOANQWYSC];Glycosyl hydrolases family

11 active sites signatures, Glycosyl Hydrol F11.2

[VATEGYFSSGS];Glycosyl Hydrol_F11.1 [PLIEYVVENF]"

/codon_start=1

/product="probable endo-1, 4-beta-xylanase B precursor"

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/db_xref="GOA:Q871B8"

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SIDGTATFYQYMSVRQKKTGGSVNNKHPDAWTRSLTLGTHNYQIVATEGYFSSGS

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Nectria haematococca, PIR:S70702"

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Db 3560 CGCAACCCGCTCATCGAATACTACTCGTGTGAGAACTTTGAACTTCAACACCCGACG 3501
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db 3500 GCGCCACCCGCTCGGGTCCGTCACCTCAGACGGCGGCTCTACGACATCTACCGCAC 3441
QY 121 GluArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db 3440 CAGCGGCTCAACAGCCCTCCATCGACGGCACCGCCACTTTTACCAGTACTGTGTCGTC 3381
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
Db 3380 CGCAGCAGAGCGTACGGCGGTAGTGTCAACATGAAGAACCACTTTGACCGCTGGACT 3321
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
Db 3320 AGTCCGGTCTCAGCTCGGCACCACTACAGATTGTGCTACCGAGGGATATTT 3261
QY 181 SerSerGlySerAlaSerIleThrVal 189
Db 3260 TCCAGTGGCAGCAGTACTATCAATGTT 3234

RESULT 14
LOCUS AR149835 1281 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6228629.
ACCESSION AR149835
VERSION AR149835.1 GI:15114426
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1281)
AUTHORS Palohelimo,M., Hakola,S., Mantyla,A., Vehmaanpera,J., Lantto,R.,
Lahtinen,T., Fagerstrom,R.B. and Suominen,P.
TITLE Xylanases, genes encoding them, and uses thereof
JOURNAL Patent: US 6228629-A 1 08-MAY-2001;
FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN
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Score: 687.00 Matches: 126
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Best Local Similarity: 60.00% Mismatches: 36
Query Match: 65.68% Indels: 22
DB: 6 Gaps: 2

US-09-990-874B-55 (1-190) x AR149835 (1-1281)

QY 1 GlnThrIle---GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
Db 273 CAGACGCTCACCAGCAGTGCACCGGCACCAATGGCTACTACTACAGCTTCTGGACC 332
QY 20 AspGlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrp 39
Db 333 GATGGCCAAAGGCAACATTCGCTTCAACCTCGAGCGGTGGCCAGTACAGCGTGACATGG 392
QY 40 SerAsnSerGlyAsnPheValGlyGlyLys----- 49
Db 393 TCTGTGAACGGCACTGGGTGGCGCAA-AGGTATGTCTCTTTAATGTTCCAGCGCTA 451
QY 50 -----GlyTrpGlnProGlyThrLysAsnLysVal 59
Db 452 TGGATGAACATAATGCTAACCTGTTAAACAGGGTGGAAACCCCGGTACCGGATACCGGTGC 511

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QY 60 IleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrp 79
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QY 80 SerArgAsnProLeuIleGluTyrThrIleValGluAsnPheGlyThrTyrAsnProSer 99
Db 572 ACCCGCAACCCGCTCATCGAGTACTACTCGTGTGAGAGCTTCGGCACTTACGACCCGTCG 631
QY 100 ThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArg 119
Db 632 ACCGGCGCCACCCGCAATGGCAGCGTACCCAGACGGCGGCACCTTCAACATCTACCGC 691
QY 120 ThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSer 139
Db 692 ACCGAGCGGCTCAACGGCCCTCCATCGAGGGCACCAAGACCTTCTACCAATACTGTCT 751
QY 140 ValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrp 159
Db 752 GTGCGCACCTCCAAAGCGCACCGCGGTACTGTTACCATGGCCCAACCACTTCAATGCTTG 811
QY 160 AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 812 AGCAGCGTGGTCTGCAGCTGGGTTCCTCATGATTATCAGATTGTGGCTACTGAGGGTTAC 871
QY 180 PheSerSerGlySerAlaSerIleThrVal 189
Db 872 TACTCGTCTGGCTCGCGGACTGTCAATGTT 901

RESULT 15
LOCUS CQ847410 1281 bp DNA linear PAT 19-AUG-2004
DEFINITION Sequence 1 from Patent EP1433843.
ACCESSION CQ847410
VERSION CQ847410.1 GI:51469070
KEYWORDS Chaetomium thermophilum
SOURCE Chaetomium thermophilum
ORGANISM Chaetomium thermophilum
REFERENCE 1
AUTHORS Palohelimo,M., Hakola,S., Maentylae,A., Vehmaanpera,J., Lantto,R.,
Lahtinen,T., Fagerstrom,R. and Suominen,P.
TITLE Novel xylanases, genes encoding them, and uses thereof
JOURNAL Patent: EP 1433843-A 1 30-JUN-2004;
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1,94e-52 Length: 1281
Score: 687.00 Matches: 126
Percent Similarity: 72.86% Conservative: 27
Best Local Similarity: 60.00% Mismatches: 36
Query Match: 65.68% Indels: 22
DB: 6 Gaps: 2

US-09-990-874B-55 (1-190) x CQ847410 (1-1281)

QY 1 GlnThrIle---GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
Db 273 CAGACGCTCACCAGCAGTGCACCGGCACCAATGGCTACTACTACAGCTTCTGGACC 332
QY 20 AspGlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrp 39
Db 333 GATGGCCAAAGGCAACATTCGCTTCAACCTCGAGCGGTGGCCAGTACAGCGTGACATGG 392
QY 40 SerAsnSerGlyAsnPheValGlyGlyLys----- 49
Db 393 TCTGTGAACGGCACTGGGTGGCGCAA-AGGTATGTCTCTTTAATGTTCCAGCGCTA 451
QY 50 -----GlyTrpGlnProGlyThrLysAsnLysVal 59
Db 452 TGGATGAACATAATGCTAACCTGTTAAACAGGGTGGAAACCCCGGTACCGGATACCGGTGC 511

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Qy      50  -----GlyTTPGlnProGlyThrLysAsnLysVal 59
Db      452  TGGAAATGAACTAAATGTCTAAGCTGTTAAACAGCGTGGAAACCCCGGTACCGATACCGTGTC 511
Qy      60  IleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTTP 79
Db      512  ATCAACTACACAGCGGACTACAGACCCCAACGCAACTCTTACCTCGCGCTCTACGGCTGG 571
Qy      80  SerArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSer 99
Db      572  ACCGCAACCCGCTGATCGAGTACTTACGTGGTCGAGAGCTTCGGCACTTACGACCCGCTCG 631
Qy      100  ThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArg 119
Db      632  ACGGGCGCCACCCGATCGGCGAGCGGTGACACCGAGCGGCGACCTACACATCTACCGC 691
Qy      120  ThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTTPSer 139
Db      692  ACGCAGCGCGTCAACGCGCCCTCCATCGAGGGCACCAGACCTTCTACCAATACTGGTCT 751
Qy      140  ValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTTP 159
Db      752  GTGGCACCTCCAAGCGCACCGCGGTACTGTTACCATGGGCCAACCACTTCAATGCTTGG 811
Qy      160  AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db      812  AGGCAGCGCTGCTGTCAGCTGGGTCCCATGATTATCAGATTGTGGCTACTGAGGGTTAC 871
Qy      180  PheSerSerGlySerAlaSerIleThrVal 189
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 Job time : 3281 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2005, 19:17:01 ; Search time 474 seconds
(without alignment)
2671.501 Million cell updates/sec

Title: US-09-990-874B-55

Perfect score: 1046

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
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- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 974 | 93.1 | 596 | 3 AAA48219 | Aaa48219 T. reesei |
| 2 | 974 | 93.1 | 596 | 6 AAD29410 | Aad29410 Trichoder |
| 3 | 974 | 93.1 | 596 | 9 AAL60925 | Aal60925 Trichoder |
| 4 | 974 | 93.1 | 596 | 9 AAL60941 | Aal60941 Trichoder |

| | | | | | |
|----|-------|------|------|-------------|--------------------|
| 5 | 948 | 90.6 | 573 | 2 AAV36098 | AAV36098 DNA seque |
| 6 | 946 | 90.4 | 1015 | 2 AAQ54775 | AAQ54775 T. reesei |
| 7 | 946 | 90.4 | 1015 | 2 AAV81332 | AAV81332 T. reesei |
| 8 | 919 | 87.9 | 822 | 2 AAV29598 | AAV29598 DNA seque |
| 9 | 687 | 65.7 | 1281 | 2 AAT71585 | AAT71585 Chaetomiu |
| 10 | 664.5 | 63.5 | 705 | 10 ABQ80364 | ABQ80364 A. fumiga |
| 11 | 648 | 62.0 | 739 | 10 ABQ80363 | ABQ80363 A. fumiga |
| 12 | 643.5 | 61.5 | 588 | 5 AAS13813 | AAS13813 DNA encod |
| 13 | 643.5 | 61.5 | 678 | 4 AAD17927 | AAI17927 Thermomyc |
| 14 | 643.5 | 61.5 | 983 | 2 AAT40742 | AAT40742 Xylanase |
| 15 | 643.5 | 61.5 | 983 | 2 AAT43010 | AAT43010 Endo-1,4- |
| 16 | 642 | 61.4 | 1239 | 12 ADJ34961 | ADJ34961 DNA encod |
| 17 | 640.5 | 61.2 | 851 | 2 AAT63044 | AAT63044 Aspergill |
| 18 | 638.5 | 61.0 | 1273 | 2 AAQ90388 | AAQ90388 Xylanase |
| 19 | 638 | 61.0 | 942 | 10 ABQ80366 | ABQ80366 A. fumiga |
| 20 | 635 | 60.7 | 1174 | 2 AAT71586 | AAT71586 Chaetomiu |
| 21 | 632.5 | 60.5 | 1047 | 12 ADJ34949 | ADJ34949 DNA encod |
| 22 | 629.5 | 60.2 | 1581 | 2 AAQ69150 | AAQ69150 Aspergill |
| 23 | 627 | 59.9 | 1002 | 10 ABQ80365 | ABQ80365 A. fumiga |
| 24 | 625.5 | 59.8 | 666 | 10 ABQ80362 | ABQ80362 A. fumiga |
| 25 | 622.5 | 59.5 | 1086 | 12 ADJ34995 | ADJ34995 DNA encod |
| 26 | 611.5 | 58.5 | 1375 | 2 AAX90405 | AAX90405 Actinomad |
| 27 | 611.5 | 58.5 | 1375 | 2 AAT64930 | AAT64930 Actinomad |
| 28 | 609.5 | 58.3 | 1068 | 12 ADJ34989 | ADJ34989 DNA encod |
| 29 | 609 | 58.2 | 927 | 2 AAQ74638 | AAQ74638 Aspergill |
| 30 | 605.5 | 57.9 | 1059 | 12 ADJ35009 | ADJ35009 DNA encod |
| 31 | 605.5 | 57.9 | 2898 | 3 AAZ46404 | Aaz46404 Penicilli |
| 32 | 605 | 57.8 | 712 | 10 ABQ80361 | ABQ80361 A. fumiga |
| 33 | 602.5 | 57.6 | 1123 | 2 AAQ74098 | AAQ74098 Humicola |
| 34 | 602.5 | 57.6 | 1123 | 2 AAQ94952 | AAQ94952 Humicola |
| 35 | 601.5 | 57.5 | 2055 | 2 AAV61455 | AAV61455 Aspergill |
| 36 | 598 | 57.2 | 1008 | 12 ADJ35015 | ADJ35015 DNA encod |
| 37 | 593 | 56.7 | 1195 | 2 AAZ28864 | Aaz28864 Streptomy |
| 38 | 593 | 56.7 | 1195 | 2 AAZ28865 | Aaz28865 Streptomy |
| 39 | 591 | 56.5 | 1047 | 12 ADJ35083 | ADJ35083 DNA encod |
| 40 | 590.5 | 56.5 | 1338 | 12 ADJ35151 | ADJ35151 DNA encod |
| 41 | 590 | 56.4 | 1044 | 12 ADJ34979 | ADJ34979 DNA encod |
| 42 | 589.5 | 56.4 | 1077 | 12 ADJ34965 | ADJ34965 DNA encod |
| 43 | 584.5 | 55.9 | 2225 | 4 AAS13689 | AAS13689 Gene enco |
| 44 | 584 | 55.8 | 576 | 10 ADK70798 | ADK70798 Streptomy |
| 45 | 581.5 | 55.6 | 1065 | 12 ADJ34999 | ADJ34999 DNA encod |

ALIGNMENTS

RESULT 1
AAA48219
ID AAA48219 standard; cDNA; 596 BP.
XX
XX
AC AAA48219;
XX
DT 15-SEP-2003 (revised)
DT 28-SEP-2000 (first entry)
XX
XX
DE T. reesei xylanase, Xyn II, coding sequence, Trx.
XX
XX
KW Xylanase; animal feed; digestion efficiency; thermostable;
KW feed pelleting; enzyme; Trx; XyTV-101; XyTV-102; Trx-103; XyTV-104;
KW XyTV-105; XyTV-106; XyTV-107; Trx-108; XyTV-109; Xyn A; Xyn B;
KW Xyn; Xyn C; Xyn I; Xyn II; ss.
XX
XX
OS Hypocrea jecorina.
XX
XX
FH Key Location/Qualifiers
CDS 23..594
FT /*tag= a
FT /partial
FT /product= "Trx"

WO200029587-A1.

25-MAY-2000.

PF 16-NOV-1999; 99WO-CA001093.
 XX
 PR 16-NOV-1998; 98US-0108504P.
 XX
 XX (IOGE-) IOGEN CORP.
 PA
 PI Sung WL, Tolan JS;
 XX
 XX
 DR WPI; 2000-387799/33.
 DR P-PSDB; AAY99680.
 XX
 PT Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological
 PT conditions.
 XX
 PS Example 1; Fig 2; 86pp; English.
 XX
 CC Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting process
 CC and to have optimum activity in the animal, the xylanase needs to have
 CC high thermostability, with optimum activity at physiological pH and
 CC temperature. Various xylanases have some properties suitable for feed
 CC applications but they lack the thermostability required to survive food
 CC pelleting. The present sequence is the coding sequence for xylanase Trx,
 CC which was derived from *Trichoderma reesei*. This coding sequence was
 CC constructed from 18 overlapping oligonucleotides: XyTV-101 (AAA48229),
 CC XyTV-102 (AAA48230), Trx-103 (AAA48231), XyTV-104 (AAA48232), XyTV-105
 CC (AAA48233), XyTV-106 (AAA48234), XyTV-107 (AAA48235), Trx-108 (AAA48236),
 CC XyTV-109 (AAA48237), XyTV-110 (AAA48238), Trx-11 (AAA48239), XyTV-2
 CC (AAA48240), Trx-3 (AAA48241), XyTV-4 (AAA48242), Trx-5 (AAA48243),
 CC (AAA48244), XyTV-7 (AAA48245), Trx-8 (AAA48246). This sequence was
 CC mutated to produce mutant xylanases with enhanced thermostability
 CC (AAY99683, AAY99684, AAY99685, AAY99686, AAY99735 and AAY99736) which
 CC would be useful for animal feeds, especially poultry and swine feed.
 CC (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 596 BP; 175 A; 131 C; 140 G; 150 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.12% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 3 Gaps: 0

US-09-990-874B-55 (1-190) x AAA48219 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
 DB 23 CAACAATACACACCGAGAACCGGTTACACACCGGTTACTTTTACAGCTATGGACGAT 82
 QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 DB 83 GGCCATGGTGGTGTACTTATACAAACGGCCGGCCGAGGCCAATTTAGGCTCAATGGTCT 142
 QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIle 60
 DB 143 AACTCCGGAACACTTCGTAGGTGGAAGAGGTTGGCAACCCGGGACCCAAATAAGGTGATC 202
 QY 61 AsnPheSerGlySerTyrAsnProAsnGlnVAnSerTyrLeuAlaValTyrGlyTrpSer 80
 DB 203 AACTTCTCTGGATCTTAATCCGAATCGGAATTCATACTTAAGCGTCTATGGCTGGTCT 262
 QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAAACCCACTGATTGATATATACATGTCGAAATTTCCGTACTTACATCCGAGTACC 322
 QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 323 GGCGCCACAAATTAGCGCAAGTCACTAGTGTGATCGATCCGTATATGATATCTACCGTACC 382

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 DB 383 CAACGGCTTAATCAGCCATCGATCATTTGGAAACCGCCACCTTTTATCATGACTCGAGTGT 442
 QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 443 AGACGTAATCATCGGAGCTCCGGTTCGGTTAAATCACTCGAATCACTTTAATGCAATGGCA 502
 QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 503 CAGCAAGGTTTACCCCTAGGTACATGATTAATCAATCGTAGCGGTGGAGGCTACTTTC 562
 QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 563 TCGAGTGGTTCGCTAGTATTACAGTGAGC 592
 RESULT 2
 AAD29410
 ID AAD29410 standard; DNA; 596 BP.
 XX
 AC AAD29410;
 XX
 DT 29-AUG-2003 (revised)
 DT 16-MAY-2002 (first entry)
 XX
 DE *Trichoderma reesei* xylanase (Trx), Xyn II DNA.
 XX
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 KW pulp manufacture; poultry; swine feed; enzyme; Xyn II; ds.
 XX
 OS *Hypocrea jecorina*.
 XX
 FH Key Location/Qualifiers
 FT CDS 23..595
 FT /*tag= a
 FT /product= "Trx Xyn II"
 FT /note= "CDS does not include start codon"
 FT /partial
 XX
 PN WO200192487-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 31-MAY-2001; 2001WO-CA000769.
 XX
 PR 31-MAY-2000; 2000US-0213803P.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Sung WL;
 XX
 DR WPI; 2002-171435/22.
 DR P-PSDB; AAE18452.
 XX
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.
 XX
 PS Example 1; Page 88; 109pp; English.
 XX
 CC The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is *Trichoderma reesei*
 CC xylanase (Trx), Xyn II DNA. (Updated on 29-AUG-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 596 BP; 175 A; 131 C; 140 G; 150 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AAD29410 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTpsAsnAsp 20
 DB 23 CAACAATAACACCGGACCGGTTACAAACCGGTTACTTTTACAGCTATTGGACGAT 82
 QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTpsSer 40
 DB 83 GGCATGTTGGTGTACTTACATACAAACCGGCGGAGCCCAATTAGCGTCAATTGGTCT 142
 QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValile 60
 DB 143 AACTCCGGAACCTTCGTAGGTGGAAGGTTGGCAACCGGACCAAAATAAGGTGATC 202
 QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTpsSer 80
 DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGCT 262
 QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAACCACCTGATTGATATACATTTGTCGAAAATTTCCGTACCTACATCCGAGTACC 322
 QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 323 GGGCCACAAAATTAGCGGAGTCACTAGTGTGATGGATCCGTATATGATATCTACCGTACC 382
 QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTpsSerVal 140
 DB 383 CAACGGGTTAATCAGCCATCGATCATTTGGAACCGCCACCTTTTATCATGTACTGGAGTGT 442
 QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTpsAla 160
 DB 443 AGACGTAAATCATCGGAGCTCCGGTTCCGTTAATCTACTGCGAATCACTTTAATGATGGCA 502
 QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 503 CAGCAAGGGTTAACCTTAGTGTACATGATGATCAATCGTACGATCGGTTGGAGGCTACTTC 562
 QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 563 TCGAGTGGTTCGCTAGTATTACAGTGAGC 592

RESULT 3

AAL60925
 ID AAL60925 standard; DNA; 596 BP.

XX AC AAL60925;

XX XX

XX DT 27-OCT-2003 (revised)

XX DT 03-SEP-2003 (first entry)

XX DE

XX Trichoderma reesei xylanase II enzyme (Trx) gene #1.

XX KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;

XX KW pulp manufacture; poultry feed; swine feed; enzyme; gene; ds.

XX XX

XX OS Hypocrea jecorina.

XX XX

XX FH Key Location/Qualifiers

XX FT 23..595

XX FT /*tag= a

XX FT /product= "T. reesei xylanase II enzyme (Trx)"

XX FT /note= "CDS does not include start codon"

XX FT /partial

XX FT

XX XX

PN WO2003046169-A2.
 XX XX
 PD 05-JUN-2003.
 XX XX
 PP 20-NOV-2002; 2002WO-CA001758.
 XX XX
 PR 21-NOV-2001; 2001US-00990874.
 XX XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX XX
 PI Sung WL;
 XX XX
 XX WPI; 2003-513647/48.
 DR P-PSDB; AAO30259.

Novel modified xylanase useful in industrial process, exhibits improved thermophilicity, alkalophilicity and expression efficiency, in comparison to a corresponding native xylanase from *Trichoderma reesei*.
 Example 1; Fig 2; 105pp; English.
 The invention relates to modified xylanase enzyme which exhibits improved thermophilicity, alkalophilicity and expression efficiency, in comparison to a corresponding native *Trichoderma reesei* xylanase (Trx). The modified xylanase is useful in an industrial process e.g. pulp manufacturing. It is useful for the bleaching of pulp, processing of precision devices and for improving digestibility of poultry and swine feed. The present sequence is *Trichoderma reesei* xylanase II enzyme encoding gene. (Updated on 27-OCT-2003 to standardise OS field)
 XX Sequence 596 BP; 175 A; 131 C; 140 G; 150 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x AAL60925 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTpsAsnAsp 20
 DB 23 CAACAATAACACCGGACCGGTTACAAACCGGTTACTTTTACAGCTATTGGACGAT 82

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTpsSer 40
 DB 83 GGCATGTTGGTGTACTTACATACAAACCGGCGGAGCCCAATTAGCGTCAATTGGTCT 142

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValile 60
 DB 143 AACTCCGGAACCTTCGTAGGTGGAAGGTTGGCAACCGGACCAAAATAAGGTGATC 202

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTpsSer 80
 DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATACCTTAAGCGTCTATGGCTGCT 262

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 263 AGAACCACCTGATTGATATACATTTGTCGAAAATTTCCGTACCTACATCCGAGTACC 322

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 323 GGGCCACAAAATTAGCGGAGTCACTAGTGTGATGGATCCGTATATGATATCTACCGTACC 382

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTpsSerVal 140
 DB 383 CAACGGGTTAATCAGCCATCGATCATTTGGAACCGCCACCTTTTATCATGTACTGGAGTGT 442

QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTpsAla 160
 DB 443 AGACGTAAATCATCGGAGCTCCGGTTCCGTTAATCTACTGCGAATCACTTTAATGATGGCA 502

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 503 CAGCAGGGTTAACCTAGGTACATCGATGGATTATCAATCGGTAGCGTGGAGGCTACTTC 562

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 563 TCGAGTGGTTCGGCTAGTATTACAGTGAGC 592

RESULT 4
 AAL60941/c
 ID AAL60941 standard; DNA; 596 BP.
 XX
 AC AAL60941;
 DT 27-OCT-2003 (revised)
 DT 03-SEP-2003 (first entry)
 XX
 DE Trichoderma reesei xylanase II enzyme (Trx) gene #2.
 XX
 KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 KW pulp manufacture; poultry feed; swine feed; enzyme; gene; ds.
 XX
 OS Hypocrea jecorina.
 XX
 PN W02003046169-A2.
 XX
 PD 05-JUN-2003.
 XX
 XX 20-NOV-2002; 2002WO-CA001758.
 PF
 XX 21-NOV-2001; 2001US-00990874.
 PR
 XX (CANA) NAT RES COUNCIL CANADA.
 PA
 XX Sung WL;
 PI
 XX WPI; 2003-513647/48.
 DR
 XX
 PT Novel modified xylanase useful in industrial process, exhibits improved
 PT thermophilicity, alkalophilicity and expression efficiency, in comparison
 PT to a corresponding native xylanase from Trichoderma reesei.
 XX
 PS Example 1; Fig 2; 105pp; English.
 XX
 CC The invention relates to modified xylanase enzyme which exhibits improved
 CC thermophilicity, alkalophilicity and expression efficiency, in comparison
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
 CC is useful for the bleaching of pulp, processing of precision devices and
 CC for improving digestibility of poultry and swine feed. The present
 CC sequence is Trichoderma reesei xylanase II enzyme encoding gene. (Updated
 CC on 27-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 596 BP; 150 A; 140 C; 131 G; 175 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,35e-94 Length: 596
 Score: 974.00 Matches: 179
 Percent Similarity: 96.32% Conservative: 4
 Best Local Similarity: 94.21% Mismatches: 7
 Query Match: 93.12% Indels: 0
 DB: 9 Gaps: 0

US-09-990-874B-55 (1-190) x AAL60941 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
 DB 578 CAACACATACACACACCGGTAACCGGTTACCAACACGGTTACTTTTACAGTATTGGACGAT 519

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSer 40
 DB 518 GGCCATGTTGGTGTGTACCTATATACAAACGGGCGGAGGCCAATTTAGCGTCAATTGGTCT 459

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrIysAsnLysValIle 60
 DB 458 AACTCCGGAACTTCGTAGGTGGAAAGGTTGGCAACCCCGGACCCAAAAATAAGGTGATC 399

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrIleuAlaValTyrGlyTrpSer 80
 DB 398 AACTTCTCTGGATCTTATATATCCGAATGGGAATTCATACTTAAGCGTCTATGGCTGTCT 339

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 338 AGAACCCTGATTTGATATATACATTTGTCGAAATTTTCGGTACCTACCAATCCGAGTACC 279

QY 101 GlyAlaThrIlyHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 278 GGGCCACAAAAATTAGCGGAAGTCACCTAGTGTAGTGGATCCGTATATATATCTACCGTACC 219

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 DB 218 CAACGGCTTAAATCAGCCATCGATCATTTGGAAACCGCCACCTTTTATCATGACTGGAGTGT 159

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 158 AGACGTAAATCATCGAGCTCCGGTTCGGTTAATCTGCGAATCACTTTAATGCATGGCA 99

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
 DB 98 CAGCAGGGTTAACCTAGGTACATCGATTATCAATCGTAGCGTGGAGGCTACTTC 39

QY 181 SerSerGlySerAlaSerIleThrValSer 190
 DB 38 TCGAGTGGTTCGGCTAGTATTACAGTGAGC 9

RESULT 5
 AAV36098
 ID AAV36098 standard; DNA; 573 BP.
 XX
 AC AAV36098;
 DT 02-SEP-1998 (first entry)
 XX
 DE DNA sequence of the specification.
 XX
 KW Family 11 xylanase; improve; thermophilicity; alkalophilicity;
 KW thermotolerance; bleach; wood pulp; processing; wheat; maize;
 KW digestibility-improving animal feed additive; starch production; mutant;
 KW ds.
 XX
 OS Synthetic.
 XX
 PN EP828002-A2.
 XX
 PD 11-MAR-1998.
 XX
 XX 05-SEP-1997; 97EP-00115412.
 XX
 XX 09-SEP-1996; 96US-00709912.
 XX
 XX (CANA) NAT RES COUNCIL CANADA.
 XX
 XX Sung WL, Yaguchi M, Ishikawa K;
 XX WPI; 1998-161100/15.
 XX
 XX Modified xylanase enzymes - useful for improving wood pulp bleaching,
 XX etc.
 XX
 PS Disclosure; Page 50; 84pp; English.
 XX
 CC The present sequence appears in the specification, which describes a
 CC method for modifying a Family 11 xylanase to improve its thermophilicity,
 CC alkalophilicity and or thermotolerance. This method comprises
 CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase


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Db 395 AACTCGGGCAACTTTTGTTCGGCGCAAGGATGGCAGCCCGGGACCAAGAACAGTAAGAC 454
QY 58 ----- 58
Db 455 TACCTACTCTTACCCCTTTTGACCAACACAGCACACACATACACATGTGACTACC 514
QY 59 -----ValleAsnPheserGly 64
Db 515 AATCATGGAATCGGATCTAACAGCTGTGTTTTTAAAAAAGGGTCATCAACTTCTCGGA 574
QY 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu 84
Db 575 AGCTACAAACCCCAACGGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTG 634
QY 85 IleGluTyrTrilleValGluAsnPheserGlyThrTyrAsnProSerThrGlyAlaThrlys 104
Db 635 ATCAGTACTACATCGTCGAGAACTTTGGCACTTACACCCGTCCACGGGGCCACCCAG 694
QY 105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
Db 695 CTGGCGAGGTCACCTCGACGGCAGCGTCTACGACATTTACCGCAGCAGCGGTCAAC 754
QY 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArg 144
Db 755 CAGCGTCCATCATCGGCACCGCACCTTTTACCAGTACTGGTCCGTCCGCGCAACCCAC 814
QY 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeu 164
Db 815 CGCTCGAGCGGCTCCGTCTACACGGCGAACCACTTCAACGGTGGGCTCAGCAAGGCGCTG 874
QY 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
Db 875 ACGTCTGGGAGGATGATTACCAAGTTGTCGGTGGAGGTACTTTAGTCTGGCTCT 934
QY 185 AlaSerIleThrValSer 190
Db 935 GCTTCCATCACCGTCAGC 952

RESULT 7
AAV81332
ID AAV81332 standard; DNA; 1015 BP.
XX AC
XX AAV81332;
XX
DT 17-OCT-2003 (revised)
DT 02-MAR-1999 (first entry)
XX
XX T. reesei xylanase II gene.
XX
XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;
XX degradation; polymer; xylan; carbohydrate; plant; paper; pulp; ss.
XX
XX Hypocrea jecorina.
XX
XX Key Location/Qualifiers
XX TATA_signal 36..42
XX /tag= a
XX CDS 176..955
XX /tag= b
XX /gene= "xln2"
XX /product= "xylanase 2"
XX /note= "CDS contains an intron"
XX sig_peptide 176..232
XX /tag= c
XX /note= "primary signal peptide sequence"
XX sig_peptide 233..275
XX /tag= d
XX /note= "propeptide sequence"
XX mat_peptide 275..952
XX /tag= e
XX intron 449..556
XX /tag= f
XX /cons_splice= (5'site:NO, 3'site:NO)

```

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XX US5837515-A.
XX PN
XX PD
XX 17-NOV-1998.
XX PF
XX 16-SEP-1993; 93US-00121436.
XX PR
XX 16-MAY-1990; 90US-00524308.
XX PR 29-MAY-1992; 92US-00889893.
XX PR 24-MAY-1993; 93WO-FI000221.
XX PR 18-JUN-1993; 93US-00078478.
XX PA (ALKO-) ALKO-YHTIOET OY.
XX
XX Paloheimo M, Nevalainen H, Saarelainen R, Fagerstroem R,
XX Suominen P;
XX
XX WPI; 1999-023453/02.
XX P-PSDB; AAW67567.
XX
XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for
XX recombinant production of the enzyme, for use in paper and pulp
XX production.
XX
XX Claim 4; Fig 3A-B; 52pp; English.
XX
XX This sequence corresponds to the gene encoding the Trichoderma reesei
XX xylanase II enzyme (xln2) which has an isoelectric point (pI) of 9. The
XX sequence was isolated by reverse transcription PCR using the primers
XX AAV81333-V81335 based on amino acid sequence derived from the N-terminal
XX of the purified protein. The encoded protein contains a 33 amino acid
XX propeptide sequence with a primary signal peptide cleavage site between
XX residues 19-20. The mature protein comprises 190 amino acids with a
XX calculated molecular weight of 20.8 kD. The enzymes are used in the
XX degradation of the polymer xylan, one of the most abundant carbohydrate
XX components in plants. This is especially useful in the paper and pulp
XX making industry. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 1015 BP; 261 A; 328 C; 240 G; 186 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.59e-91 Length: 1015
Score: 946.00 Matches: 179
Percent Similarity: 80.97% Conservative: 4
Best Local Similarity: 79.20% Mismatches: 7
Query Match: 90.44% Indels: 36
DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x AAV81332 (1-1015)
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db 275 CAGACGATTTCAGCCCGGACGCGGTACACACACGGCTACTTCTACTGTGTAAGACGAT 334
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 335 GGCCACGGCGGCGTGACGTACCAATGGTCCCGCGGCGAGTTCTCCGTCACTGGTCC 394
QY 41 AsnSerGlyAsnPheserValGlyGlyGlyTyrGlnProGlyThrIleAsnIle 58
Db 395 AACTCGGGCAACTTTTGTTCGGCGCAAGGATGGCAGCCCGGGACCAAGAACAGTAAGAC 454
QY 58 ----- 58
Db 455 TACCTACTCTTACCCCTTTTGACCAACACAGCACACACATACACATGTGACTACC 514
QY 59 -----ValleAsnPheserGly 64
Db 515 AATCATGGAATCGGATCTAACAGCTGTGTTTTTAAAAAAGGGTCATCAACTTCTCGGA 574
QY 65 SerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu 84
Db 575 AGCTACAAACCCCAACGGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTG 634

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QY 85 IleGluTyrTrpValGluAlaPheGlyThrTyrAsnProSerThrGlyAlaThrIys 104
DB 635 ATCCAGTACTACATCGTCGAGACTTTGGACCTTACACCCGTCACCGGGGCCACCCAG 694
QY 105 HisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsn 124
DB 695 CTGGCGAGGTCACCTCCGACGGCAGCGCTTACGACATTTACCGCAGCGGCTCAAC 754
QY 125 AlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArg 144
DB 755 CAGCCGTCCTCATCTCGGCACCGCCACCTTTACGACTACTGGTCGTCGCCGCAACCC 814
QY 145 ArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeu 164
DB 815 CGCTCGAGCGGCTCGTCAACACGCGGACCCACTTCAAGCGTGGCTCAGCAAGGCTG 874
QY 165 ThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySer 184
DB 875 ACGCTCGGACGATGATACAGATTGTTCCGCTGGAGGGTTACTTTAGCTCTGGCTCT 934
QY 185 AlaSerIleThrValSer 190
DB 935 GCTTCCATCCCGTCAGC 952

RESULT 8

ID AAV29598 standard; DNA; 822 BP.

AC AAV29598;

DT 02-SEP-1998 (first entry)

DE DNA sequence of the specification.

KW Regulatory sequence; cellulase cbhl gene; mass production;

KX Humicola insolens; endo-glucanase NCE4; ds.

OS Trichoderma viride.

Key Location/Qualifiers

CDS 14..812

FT /*tag= a

FT /note= "contains an intron"

FT sig_peptide 14..112

FT /*tag= b

FT mat_peptide 113..809

FT /*tag= c

FT intron 286..412

FT /*tag= d

XX WO9811239-A1.

XX 19-MAR-1998.

XX 16-SEP-1997; 97WO-JP003268.

XX 13-SEP-1996; 96JP-00243695.

XX (MEIJ) MEIJI SEIKA KAISHA LTD.

XX Watanabe M, Moriya T, Aoyagi K, Sumida N, Murakami T;

XX WPI; 1998-250959/22.

XX P-PSDB; AAW57422.

XX regulatory sequence for Trichoderma viride derived cellulase cbhl gene -

XX for producing Humicola insolens derived endo-glucanase.

XX Disclosure; Page 57-59; 92pp; Japanese.

XX The present sequence appears in the specification. The specification

XX describes a new regulatory sequence for Trichoderma viride derived

CC cellulase cbhl gene and the establishment of a system for mass producing
CC cellulase in moulds such as T. viride. As the regulatory sequence of cbhl
CC genes originating in T. viride can highly express objective proteins,
CC proteins such as cellulase can be expressed. An expression vector
CC containing the regulatory sequence and Humicola insolens derived endo-
CC glucanase NCE4 DNA was produced, and used to produce endo-glucanase at 15
CC grams per litre

SQ Sequence 822 BP; 178 A; 280 C; 211 G; 153 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,64e-88 Length: 822
Score: 919.00 Matches: 176
Percent Similarity: 77.68% Conservative: 5
Best Local Similarity: 75.54% Mismatches: 9
Query Match: 87.86% Indels: 43
DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x AAV29598 (1-822)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAsp 20
DB 113 CAGACGATTTCAGCCCGCAGCGGTACACACGCGTACTTCTACTCGTACTGACACGAC 172
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 173 GGCACGCGGCGGTGACGTACACCAATGGCCCGCGCCAGTTCTCCGTCACTGGTCC 232
QY 41 AsnSerGlyAsnPheValGlyGlyLeuGlyTyrGlnProGlyThrLys----- 56
DB 233 AACTCGGGCAACTTTGTTCGCGCGCAAGGGATGGCAGCCCGCCACCAAGNACAAGTAAGAC 292
QY 56 ----- 56
DB 293 TATATACACCCCACTTCTGACCAAAACCCCTATCCACGACAGATATATAAACCAAGG 352
QY 57 -----AsnLys 58
DB 353 GCGTGATTATCATGGAGAGAGAGAGTGTGTGATCTATACGGTTTTTGTCTGAAACAAG 412
QY 59 -ValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrG 78
DB 413 GGTCACTCAACTTCTCGGGCACTTACACCCCAACGCAACAGCTTACCTCTCCGTGTACGG 472
QY 78 YTrpSerArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnPr 98
DB 473 CTGGTCGCGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCTTACACCC 532
QY 98 oSerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCy 118
DB 533 GTCCACCGGCGCCACCAAGCTGGCGAGGTGACGTGCGACGGCAGCGCTTACGACATCTA 592
QY 118 sArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTr 138
DB 593 CCGCAGCGCAGCGGTCAACCCAGCGCTCATCGAGGCGCACCTCCACCTTTTACCAAGTAC 652
QY 138 pSerValArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAl 158
DB 653 GTCCGTCGCGCGCACCCACCGCTCCAGCGGCTCCGTCAACACCGGCAACCACTTCAACGC 712
QY 158 aTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluG 178
DB 713 GTGGGCTCGCAGCGGCTGACGTGGGCACCATGGATTACAGATTGTTGCCGTGGAGGG 772
QY 178 YTrpPheSerSerGlySerAlaSerIleThrValSer 190
DB 773 CTACTTTAGTCTGCGTCTGCTTCCATCCATCCCGTCAGC 809

RESULT 9

AAAT71585

ID AAT71585 standard; DNA; 1281 BP.

XX AAT71585;

xx 17-OCT-2003 (revised)
 DT 15-SEP-1997 (first entry)
 XX Chaetomium thermophilum xylanase A xlnA gene.
 DE Xylanase A; xlnA gene; pulp; bleaching; baking; ss.
 KW Chaetomium thermophilum; CBS 730.95 (ALKO4265).
 XX
 OS
 XX
 XX Key Location/Qualifiers
 FT exon 195..423
 FT sig_peptide 195..252
 FT intron 424..482
 FT exon 483..1039
 FT /*tag= c
 PN WO9722692-A1.
 XX
 XX 26-JUN-1997.
 XX 17-DEC-1996; 96WO-FI000671.
 XX 18-DEC-1995; 95US-0008746P.
 PR 28-JUN-1996; 96US-0020839P.
 XX
 XX (PRIM-) PRIMALCO LTD.
 XX Paloheimo M, Hakola S, Maentylae A, Vehmaanperae J, Lantto R;
 PI Lahtinen T, Fagerstrom R, Suominen P;
 XX
 DR WPI; 1997-341683/31.
 DR P-PSDS; AAW18115.
 XX
 XX Nucleic acid encoding new xylanase(s) from Chaetomium thermophilum -
 PT useful for treating wood pulp, animal feed and flour, e.g. to facilitate
 PT bleaching.
 XX
 XX Claim 1; Page 42-43; 76pp; English.
 XX
 XX The Chaetomium thermophilum xlnA gene (AA71585) codes for novel xylanase
 CC A (AAW18115), an enzyme that has a temperature optimum of over 50 deg C
 CC at pH 4-8 (partic. pH 5-7). Plasmid pALK1026 contg. the xlnA gene has
 CC been deposited as DSM 11021. The xlnA, xlnB (see also AAT71586) and xlnC
 CC (see also AAT71587) genes were isolated from a C. thermophilum CBS 730.95
 CC genomic library by hybridisation to the Trichoderma reesei xln2 gene. The
 CC isolated genes can be used for recombinant prodn. of C. thermophilum
 CC xylanases in transformed host cells (esp. T. reesei) for use in enzyme-
 CC aided bleaching of wood pulp and in methods of modifying plant biomass,
 CC e.g. as a feed additive or in baking. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 1281 BP; 308 A; 385 C; 324 G; 264 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 2.63e-63 Length: 1281
 Score: 687.00 Matches: 126
 Percent Similarity: 72.86% Conservative: 27
 Best Local Similarity: 60.00% Mismatches: 36
 Query Match: 65.68% Indels: 22
 DB: 2 Gaps: 2
 XX
 US-09-990-874b-55 (1-190) x AAT71585 (1-1281)
 Qy 1 GlnThrIle---GlnProGlyThrHisAspGlyTyrPheTyrSerTyrTyrAsn 19
 Db 273 CAGACGCTCCACCGAGTGGCCCGGACCCCAATGGCTACTACTACAGCTTCTGGACC 332
 Qy 20 AspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyr 39

Db 333 GATGGCCAAAGGCAACATTCGCTTCAACCTCGAGAGCGGTGGCCAGTACAGCGTGACATGG 392
 Qy 40 SerAsnSerGlyAsnPheValGlyGlyLys-----GlyTyrGlnProGlyThrLysAsnLysVal 59
 Db 393 TCTGGTAACGGCACTGGGTGGGGCAA-AGGTATGTCTCTTTAAATGTTTCCAGCGCTA 451
 Qy 50 -----GlyTyrGlnProGlyThrLysAsnLysVal 59
 Db 452 TGGAAATGAACATAAATGCTAACTGTTAAACAGGCTGGAAACCCCGTACCGATAACCGTGC 511
 Qy 60 IleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyr 79
 Db 512 ATCAACTACACAGCCGACTACAGACCCACCGCAACTCTTACCTCGCGCTCTACGGTGG 571
 Qy 80 SerArgAsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSer 99
 Db 572 ACCGGCAACCCGCTGATCGAGTACTAGTGTCTGAGAGCTTCGGCACTTACGACCCGCTG 631
 Qy 100 ThrGlyAlaThrLysHisGlyValThrSerAspGlySerValTyrAspIleCysArg 119
 Db 632 ACGGGGCGCCACCCGATGGCGAGCTGACCCGCGCGGACCTTACCAACATCTACCGC 691
 Qy 120 ThrGlnArgValAsnAlaProSerIleGlyGlyThrAlaThrPheTyrGlnTyrTyrSer 139
 Db 692 ACGCAGCGCTCAACGCGCCCTCCATCGAGGGCACCAGACCTTCTACCAATACTGTCT 751
 Qy 140 ValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyr 159
 Db 752 GTGGCACTCCAGCGCACCGCGGTACTGTACCATGGCCCAACCACTTCAATGCTTG 811
 Qy 160 AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGlyTyr 179
 Db 812 AGCGAGCGTGTCTCGCAGCTGGGTTCCTCATGATATCAGATTGTGGCTACTAGGGTTAC 871
 Qy 180 PheSerSerGlySerAlaSerIleThrVal 189
 Db 872 TACTCGTCTGGCTCGCGCACTGTCAATGTT 901
 XX
 RESULT 10
 ABQ80364
 ID ABQ80364 standard; cDNA; 705 BP.
 AC ABQ80364;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE A. fumigatus AFXYL2 cDNA.
 XX
 KW Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
 KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
 KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
 KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
 KW glyceride; starch; maltodextrin; oxidized phenolic compound;
 KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
 KW textile; tea liquor; cleaning ability; ss.
 XX
 OS Aspergillus fumigatus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..705
 FT /*tag= a
 FT /product= "Xylanase 2"
 XX
 PN WO2003012071-A2.
 XX
 PD 13-FEB-2003.
 XX
 XX 05-AUG-2002; 2002WO-US024842.
 PF
 XX 03-AUG-2001; 2001US-0309870P.
 PR
 XX (ELIT-) ELITRA PHARM INC.
 PA
 XX

CC phytase, beta-galactosidases, invertase, lipase, alpha-amylase, laccase,
 CC polygalacturonase or xylanase. Compositions comprising the tannase are
 CC useful for modulating the amount of compounds that comprise a gallate
 CC ester linkage in a composition. Compositions comprising cellulase are
 CC useful for modulating the amount of cellulose in a composition.
 CC Compositions comprising glucose oxidase are useful for modulating the
 CC amount of glucose or oxygen in a composition. Compositions comprising
 CC phytase are useful for modulating the amount of myo-inositol phosphates
 CC in a composition. Compositions comprising beta-galactosidases are useful
 CC for modulating the amount of lactose in a composition. Compositions
 CC comprising sucrase or invertase are useful for modulating the amount of
 CC sucrose in a composition. Compositions comprising lipase are useful for
 CC modulating the amount of glyceride in a composition. Compositions
 CC comprising alpha-amylases are useful for modulating the amount of
 CC starches or maltodextrins in a composition. Compositions comprising
 CC laccase are useful for modulating the amount of oxidized phenolic
 CC compounds in a composition. Compositions comprising polygalacturonases
 CC are useful for modulating the amount of high or low molecular weight
 CC polygalacturonic acid chains in a composition. Compositions comprising
 CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
 CC in a composition. The A. fumigatus proteins and corresponding DNA's are
 CC useful in various industries such as those involved in the making of food
 CC and feed, beverages, textiles and detergents. The DNA's are useful to
 CC express recombinant enzymes for characterization, modification or
 CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
 CC to identify duplicated genes of paralogs having the same or similar
 CC biochemical activity and/or function, to compare with nucleic acid
 CC sequence of other related or distant fungal organisms to identify
 CC potential orthologous enzyme genes, for selecting and making oligomers
 CC for attachment to a nucleic acid array for examination of expression
 CC patterns, and to raise anti-protein antibodies. The polypeptide having
 CC tannase activity increases the yield of tea liquor from tea leaves,
 CC improves the colour, flavour and health benefits of tea products,
 CC particularly an instant tea product. The polypeptide having cellulase
 CC activity enhances cleaning ability of detergent compositions

XX Sequence 739 BP; 158 A; 235 C; 195 G; 151 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,84e-59 Length: 739
 Score: 648.00 Matches: 118
 Percent Similarity: 72.50% Conservative: 27
 Best Local Similarity: 59.00% Mismatches: 38
 Query Match: 61.95% Indels: 17
 DB: 10 Gaps: 1

US-09-990-874B-55 (1-190) x ABQ80363 (1-739)

QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
 DB 136 ACCGCTGGAAACACGGCTACTACTCTCTGAGCTGATGGCGCGGACGTGACC 195
 QY 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
 DB 196 TACACCAATGGCGCGGTGCTCGTACTCCGTCACTGGAGGAGCACTGGCGCACTTTGTC 255
 QY 47 GlyGlyLysGlyTyrGlnProGlyThr----- 55
 DB 256 GGTGGAAGGGCTGGAAACCTCGAAGCGGTAGTACCGAGCTTTGTCACTGGATGTG 315
 QY 56 -----LysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnG1 70
 DB 316 CAGACCTGGCTGACAGAGTAGACCACTCACTACGGAGGACGCTTCACCCAGCGG 375
 QY 70 YAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGluTyrTyrIleVa 90
 DB 376 CAATGGCTACCTGGCTGTCTACGGCTGGACCAACCCCTTGATTGAGTACTACTGTTGT 435
 QY 90 IclAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSe 110
 DB 436 TGAGTCGTATGTATACATACACCCCGGACGCGCGGTACCTTCAGGGGCACTGTCAACAC 495
 QY 110 rAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGlu1 130

DB 496 CGACGGTGCACTTACAAACATCTACACGCCGCTTGCTACATGTCTCCTCATCGAAGG 555
 QY 130 yThAlaThrPheTyrGlnTyrTrpSerValArgArgAsnArgArgSerSerGlySerVa 150
 DB 556 CACCAAGACCTTCACCCAGTACTGCTGTGGGCACTCCCAAGCGTACCGGCGGCACTGT 615
 QY 150 lAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMeAs 170
 DB 616 CACCATGGCCAAACCACTTCAACGCCCTGGAGCAGACTGGCACTGAACCTGGGAACCTCA 675
 QY 170 pTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
 DB 676 CTACCAGATTGTGCGCACTGAGGTTACCAAGCAGCAGCGGATCTGCTTCCATCACTGTC 733

RESULT 12

AA513813
 ID AA513813 standard; DNA; 588 BP.

XX AA513813;

XX 18-DEC-2001 (first entry)

XX DNA encoding Thermomyces lanuginosus xylanase A.

XX Xylanase A; plant cell wall; baking; cereal; starch production; wood;
 KW wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; ds.

XX Thermomyces lanuginosus.

XX WO200166711-A1.

XX 13-SEP-2001.

XX 08-MAR-2001; 2001WO-IB000426.

XX 08-MAR-2000; 2000GB-00005595.

XX 27-JUN-2000; 2000GB-00015751.

XX (DANI-) DANISCO AS.

XX Sibbesen O, Sorensen JF;

XX WPI; 2001-596834/67.

PT Novel variant xylanase polypeptide or its fragment useful for degrading
 or modifying plant cell wall, comprises amino acid modifications such
 PT that the polypeptide has altered sensitivity to xylanase inhibitor.

Dislosure; Page 64; 70pp; English.

XX The invention relates to a variant xylanase polypeptide (I) or its
 fragment having xylanase activity, comprising one or more amino acid
 CC modifications such that (I) or its fragment has an altered sensitivity to
 CC a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or
 CC its coding sequence (II) is useful for degrading or modifying plant cell
 CC wall or for processing a plant material by contacting the plant cell wall
 CC or plant material with (I) or (II). (I) is useful for modifying plant
 CC materials, and in baking, processing cereals, starch production,
 CC processing wood and enhancing the bleaching of wood pulp. (I) is useful
 CC for altering the viscosity derived from the presence of hemicellulose or
 CC arabinoxylan in a solution or system comprising plant cell wall material.
 CC (I) is useful for preparing a foodstuff such as bread, pretzels,
 CC tortillas, cakes, cookies, biscuits or crackers. The present sequence
 CC represents the coding sequence of Thermomyces lanuginosus xylanase A as
 CC described in the method of the invention

XX Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.12e-59 Length: 588
 Score: 643.50 Matches: 117
 Percent Similarity: 74.87% Conservative: 26

Best Local Similarity: 61.26% Mismatches: 47
 Query Match: 61.52% Indels: 1
 DB: 5 Gaps: 1

US-09-990-874B-55 (1-190) x AAS13813 (1-588)

```

Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db 4 CAGACAACCCCACTCGAGGGCTGGCAGCATGGTATTACTATTCCTGGTGGAGTGAC 63

Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 64 GGTGGAGCGCAGCCACGATACCACTCGAAGCGCGCATCTAGAGATGAGCTGGGA 123

Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
Db 124 GATGGCGGTAACTCGTGGTGGAAAGGGCTGGAAACCCCGGCTGACGCAAGACCATC 183

Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
Db 184 CACTTTGAGGGTGTATTACGAGCAACGCAACAGCTACTTGGCGTCTACGGTTGGACC 243

Qy 81 ArgAsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 244 CGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCCTATGATCCTTCCTCC 303

Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db 304 GGTGCTACCGATCTAGGAACGTGCGAGTCGCGAGCGTAGCATCTATCGACTCGGCAAGACC 363

Qy 121 GlnArgValAsnAlaProSerIleGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
Db 364 ACTCGCGTCAACGCACTAGCATCGACGCGCAACCCCAACCTTCGACCAATCTCTGGTCGCTC 423

Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
Db 424 CGCAGGAGCAACGCGCAGCGGTACTCGTCCAGACGGCGCTGCGCACTTCGACGCCCTGGGCT 483

Qy 161 ArgGlnGlyLeuThrLeu--GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 484 CGCGCTGTTTGAATGTCACGGTGACCGTACTACTACAGATCGTTTGCACGAGGGCTTAC 543

Qy 180 PheSerSerGlySerAlaSerIleThrValSer 190
Db 544 TTCAGCAGCGGTATGCTCGCATCACCGTGTCT 576

```

RESULT 13

AAD17927

AC AAD17927 standard; DNA; 678 BP.

AC AAD17927;

XX 10-DEC-2001 (first entry)

DT Thermomyces lanuginosus codon optimised xylanase gene.

XX Xylanase; Pichia cell; heterologous nucleotide; codon optimisation; ds.

XX Thermomyces lanuginosus.

OS Synthetic.

XX WO200166693-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-DK000154.

XX 10-MAR-2000; 2000DK-00000392.

XX 15-MAR-2000; 2000DK-00000419.

XX (NOVO) NOVOZYMES AS.

XX Takagi S, Terui Y, Teutsuni N, Taira R;

PI

XX

DR WPI; 2001-582273/65.

XX

PT Novel Pichia cell useful for producing polypeptide of interest, comprises a copy of heterologous nucleotide sequence encoding polypeptide of interest.

XX

XX Claim 14; Page 38-39; 61pp; English.

XX

CC The invention relates to a Pichia cell comprising at least one copy of heterologous nucleotide sequence encoding a polypeptide of interest, where the codon usage of the sequence has been adjusted to match the preferred codon usage of P. methanolica. The invention also relates to a method for producing high yields of heterologous codon optimised polypeptide in a Pichia cell. The Pichia cell is useful for producing a polypeptide of interest, where the polypeptide is encoded by a nucleotide sequence heterologous to P. methanolica. The present sequence is Thermomyces lanuginosus codon optimised xylanase gene which is the heterologous DNA used in the invention

XX

SQ Sequence 678 BP; 180 A; 89 C; 152 G; 257 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,97e-59 Length: 678
 Score: 643.50 Matches: 117
 Percent Similarity: 74.87% Conservative: 26
 Best Local Similarity: 61.26% Mismatches: 47
 Query Match: 61.52% Indels: 1
 DB: 4 Gaps: 1

US-09-990-874B-55 (1-190) x AAD17927 (1-678)

Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20

Db 94 CAACAACCTCCAAATTCGAAGGTGGCATGATGTTATTATTATTCCTGGTGGCTCAT 153

Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40

Db 154 GGTGGTGTCTCAAGCTACTTATCTAATAATTTAGAAGGTGGTACTTAAATTTCTTGGGGT 213

Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60

Db 214 GATGGTGGTAAATTTAGTTGGTGGTAAAGGTGGAAATCCAGGTTTAAATGCAAGAGCTATT 273

Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80

Db 274 CATTTTGAAGGTGTTTATCAACCAATGGTAAATCTTATTATAGCTGTTTATGGTTGGACT 333

Qy 81 ArgAsnProLeuIleGlyTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100

Db 334 AGAAATCCATTAGTTGAATATATATTGTTGAAAAATTTGGTACTTATGATCCATCTTCT 393

Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120

Db 394 GGTGCTACTGATTTAGGTACTGTTGAATGTGATGGTCTATTATTAGATTAGGTAAATAA 453

Qy 121 GlnArgValAsnAlaProSerIleGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140

Db 454 ACTAGAGTTAATGCAACCATCTATTGTATGGTACTCAAACTTTCGATCATATATGGTCTGTT 513

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Db 514 AGACAAGATAAAAGAACTTCTGCTACTGTTCAAACCTGGTGTCTCATTTTCGATGCTGGGCT 573

Qy 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179

Db 574 AGAGCTGGTTTGAATGTTAATGGTGGTCAATTTATTATCAAAATTTGTGCAACGAGGTTAT 633

Qy 180 PheSerSerGlySerAlaSerIleThrValSer 190

Db 634 TTCCTCTCTGTTTATGCTAGAAATTACTGTGCT 666

RESULT 14

AAT40742
 ID AAT40742 standard; cDNA; 983 BP.
 AC AAT40742;
 XX
 DT 21-MAY-1997 (first entry)
 XX
 DE Xylanase coding sequence.
 XX
 KW Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermosascus;
 KW Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia;
 KW Byssoschlamus; Paecilomyces; animal feed additive; in-vivo breakdown;
 KW plant cell wall; growth rate; feed conversion; ss.
 XX
 OS Thermomyces lanuginosus.
 XX
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 31..708
 FT /*tag= a
 FT /product= "xylanase"
 XX
 FN WO9623062-A1.
 XX
 XX
 PD 01-AUG-1996.
 XX
 PF 26-JAN-1996; 96WO-DK000046.
 XX
 PR 26-JAN-1995; 95DK-00000094.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Hansen PK, Wagner P, Muellertz A, Knap IH;
 XX
 DR WPI; 1996-454790/45.
 DR P-PSDB; AAW01112.
 XX
 PT Fungal xylanase preps. for use as animal feed additives - and DNA
 PT construct for producing recombinant Thermomyces xylanase.
 PS Claim 5; Page 45-46; 69pp; English.
 CC
 CC This sequence represents the coding sequence for the xylanase from
 CC Thermomyces lanuginosus strain DSM 4109. The encoded xylanase, and
 CC xylanases derived from Humicola, Thermosascus, Chaetomium, Mucor,
 CC Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssoschlamus or
 CC Paecilomyces strains can be used in the monocomponent xylanase
 CC preparations of the invention. The xylanase preparations and the
 CC recombinant Thermomyces xylanase are useful as animal feed additives,
 CC which promote in-vivo breakdown of plant cell wall material and thus
 CC improve digestibility, growth rate and/or feed conversion
 XX
 SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.1e-59 Length: 983
 Score: 643.50 Matches: 117
 Percent Similarity: 74.8% Conservative: 26
 Best Local Similarity: 61.26% Mismatches: 47
 Query Match: 61.52% Indels: 1
 DB: 2 Gaps: 1
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 DB 124 CAGACAACCCCACTCGGAGGCTGGCAGCATGGTATTACTATTCTCGTGGAGTGAC 183
 QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 DB 184 GGTGGAGCGCAGCCGACCTGACCACTGGAGCGGCACCTACGAGATCAGCTGGGA 243
 QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
 DB 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60

DB 244 GATGCGGTAACTCGTCGTGGTGGAAAGGGCTGGAAACCCCGCCCTGAACGCAAGACCCATC 303
 QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
 DB 304 CACTTTGAGGTGTTTACAGCCAAACGCAACAGCTACCTTGGTCTACGGTTGGACC 363
 QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 DB 364 CGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCCTATGATCCTTCTCTCC 423
 QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 DB 424 GGTGCTACCGATCTAGGAACTGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC 483
 QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 DB 484 ACTCGGTCACAGCCACCTAGCATCGAGCGCACCCCAACCTTCGACCAATATCTGGTCGTC 543
 QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 DB 544 CGCCAGGACAAGCGCACCGGTTACCGTCCAGAGCGGCTGCCACTTCGAGCGCTGGGCT 603
 QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
 DB 604 CGCGCTGGTTTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGAGGGGTAC 663
 QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
 DB 664 TTCAGCAGCGGTATGCTCGCATCACCCTTGCT 696
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 ID AAT43010 standard; cDNA; 983 BP.
 XX
 AC AAT43010;
 DT 16-OCT-2003 (revised)
 DT 22-FEB-1997 (first entry)
 XX
 DE Endo-1,4-beta-D-xylanase gene.
 XX
 KW Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
 KW Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
 XX flour; baking; dough; ss.
 OS Thermomyces lanuginosus; (strain DSM 4109).
 FH Key Location/Qualifiers
 FT 5'UTR 1..30
 FT /*tag= a
 FT CDS 31..708
 FT /*tag= b
 FT /product= "Endo-1,4-beta-D-xylanase"
 FT /note= "EC-3.2.1.8"
 FT 3'UTR 709..983
 FT /*tag= c
 XX
 XX WO9632472-A1.
 XX
 PD 17-OCT-1996.
 XX
 PF 11-APR-1996; 96WO-DK000171.
 XX
 PR 11-APR-1995; 95DK-00000435.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Jorgensen OB, Si JO, Jakobsen TS;
 XX
 DR WPI; 1996-477123/47.
 DR P-PSDB; AAW05187.
 XX
 PT Bread improving additive contg. xylanase from Thermomyces - and opt.

PT alpha-amylase, increases volume, improves anti-staling properties etc.
XX
PS
XX
XX Claim 7; Page 30-31; 41pp; English.
XX
CC The sequence encodes an endo-1,4-beta-D-xylanase from *Thermomyces*
CC *lanuginosus* (*Hemicolla lanuginosa*), which may be used as a bread-
CC improving additive. The enzyme may be expressed recombinantly from a
CC plasmid pYES2.0 vector in *Saccharomyces cerevisiae* DSM 10133 (claimed),
CC and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,
CC optionally along with other enzymes (amylase, maltogenase, lipase,
CC cellulase, hemicellulase, pentosanase, glucose-oxidase, lactase,
CC protease and/or peroxidase). The enzyme combines particularly well with
CC amylolytic enzymes, and may be used to improve baking properties of flour
CC and/or dough, by increasing volume and improving texture, flavour, crumb
CC softness, freshness and anti-staling properties, while improving dough
CC machinability and stability. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.1e-59 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: Gaps: 2
US-09-990-874B-55 (1-190) x AAT43010 (1-983)
QY 1 GlnThrIleGlnProGlyThrGlyThiAspGlyTyrPheTyrSerTyrTirAsnAsp 20
DB 124 CAGACACCCCCCACTCGGCGGGCTGGCAGCATGGTTATTACTATCTCTGGTGGAGTGAC 183
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTirPser 40
DB 184 GGTGGAGCGCAGGCGCAGGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGA 243
QY 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 244 GATCGCGGTAACTCTGCTGGTGGAAAGGGCTGGAAACCCCGGCCCTGGAACGGAAGAGCCATC 303
QY 61 AsnPheSerGlySerTyrAsnPheAsnGlyAsnSerTyrLeuAlaValTyrGlyTirPser 80
DB 304 CACTTTCAGGGGTGTACACGCAACCGCAACAGCTACCTTTCGGTCTACGGTTGGACC 363
QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 364 CGCAACCGCTGTGTCGAGTATTACATCGTCGAGAACCTTGGCACCTATGATCTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 424 GGTGCTACCGATCTAGGAACCTGTGAGTGGACGGTAGCATCTATCGACTCGGCAAGACC 483
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTirPserVal 140
DB 484 ACTCGCTCAACGCACTAGCATCGACGGCACCCCAACCTTCGACCAATACTGTCGGTCC 543
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTirPala 160
DB 544 CGCCAGGACAAGCGCACCGGGTACCGTCCAGACGGGCTGCCACTTCGACGCTGGGCT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 604 CGCGCTGGTTTGAATGTCAACGGTGACCCACTACTACCAAGATCGTTGCAACGGAGGGCTAC 663
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 664 TTCAGCAGCGGCTATGTCTCGCATCACCGTTGCT 696

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 00:18:57 ; Search time 3753 Seconds
(without alignments)
2368.651 Million cell updates/sec

Title: US-09-990-874B-55
Perfect score: 1046
Sequence: 1 QTIQGRGYHDGYFSYWN.....YQIVAVEGYFGSSASITVS 190

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n model -DEV=xlp
-Q=/cgn2_1/USPRO_pool_p/US9990874/runat_29122005_095048_5092/app query.fasta_1.327
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0990874 @CGN 1 1 8010 @runat_29122005_095048_5092 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
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| 2 | 932 | 89.1 | 799 | 6 | CB898036 |
| 3 | 877 | 83.8 | 768 | 7 | CF881056 |
| 4 | 877 | 83.8 | 822 | 6 | CB907827 |
| 5 | 680.5 | 65.1 | 738 | 6 | CD464145 |
| 6 | 658.5 | 63.0 | 860 | 8 | DR637934 |
| 7 | 658.5 | 63.0 | 883 | 8 | DR643290 |

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|----|-------|------|-----|---|----------|----------|-----------|
| 8 | 640.5 | 61.2 | 680 | 8 | DR707969 | DR707969 | Asn_08783 |
| 9 | 640.5 | 61.2 | 746 | 8 | DR701170 | DR701170 | Asn_00615 |
| 10 | 638 | 61.0 | 746 | 6 | CB901964 | CB901964 | trf028xi |
| 11 | 638 | 61.0 | 746 | 7 | CF871731 | CF871731 | trf028xi |
| 12 | 639.5 | 60.2 | 664 | 8 | DR705641 | DR705641 | Asn_05863 |
| 13 | 623.5 | 59.6 | 682 | 8 | DR702584 | DR702584 | Asn_02201 |
| 14 | 623 | 59.6 | 750 | 9 | AQ160254 | AQ160254 | mgx50003L |
| 15 | 622.5 | 59.5 | 712 | 7 | CV496238 | CV496238 | 73987.1 C |
| 16 | 616 | 58.9 | 743 | 7 | CF865758 | CF865758 | trf003xb |
| 17 | 616 | 58.9 | 802 | 6 | CB895680 | CB895680 | trf003xb |
| 18 | 609.5 | 58.3 | 772 | 7 | CN133022 | CN133022 | Ox1_9_D10 |
| 19 | 609.5 | 58.3 | 921 | 6 | CD458837 | CD458837 | FG08_04b1 |
| 20 | 608.5 | 58.2 | 639 | 8 | DR624928 | DR624928 | EST101505 |
| 21 | 608.5 | 58.2 | 686 | 8 | DR624738 | DR624738 | EST101486 |
| 22 | 608.5 | 58.2 | 719 | 8 | DR631520 | DR631520 | EST102164 |
| 23 | 608.5 | 58.2 | 733 | 8 | DR630899 | DR630899 | EST102102 |
| 24 | 608.5 | 58.2 | 739 | 8 | DR624376 | DR624376 | EST101450 |
| 25 | 608.5 | 58.2 | 749 | 8 | DR623097 | DR623097 | EST101322 |
| 26 | 608.5 | 58.2 | 763 | 8 | DR624330 | DR624330 | EST101445 |
| 27 | 608.5 | 58.2 | 784 | 8 | DR628641 | DR628641 | EST101876 |
| 28 | 608.5 | 58.2 | 801 | 8 | DR631291 | DR631291 | EST102141 |
| 29 | 608.5 | 58.2 | 807 | 8 | DR621776 | DR621776 | EST101190 |
| 30 | 608.5 | 58.2 | 809 | 8 | DR627394 | DR627394 | EST101752 |
| 31 | 608.5 | 58.2 | 842 | 8 | DR630275 | DR630275 | EST102040 |
| 32 | 608.5 | 58.2 | 886 | 8 | DR621753 | DR621753 | EST101188 |
| 33 | 608.5 | 58.2 | 891 | 8 | DR632055 | DR632055 | EST102218 |
| 34 | 608.5 | 58.2 | 916 | 8 | DR622008 | DR622008 | EST101213 |
| 35 | 606.5 | 58.0 | 729 | 8 | DR629975 | DR629975 | EST102010 |
| 36 | 606.5 | 58.0 | 763 | 8 | DR623625 | DR623625 | EST101375 |
| 37 | 602.5 | 57.6 | 741 | 8 | DR625790 | DR625790 | EST101591 |
| 38 | 600.5 | 57.4 | 882 | 8 | DR037502 | DR037502 | 49478.2 L |
| 39 | 593.5 | 56.7 | 708 | 8 | DR631672 | DR631672 | EST102180 |
| 40 | 591.5 | 56.5 | 675 | 8 | DN588726 | DN588726 | 49478.1 L |
| 41 | 589.5 | 56.4 | 670 | 8 | DR701228 | DR701228 | Asn_00686 |
| 42 | 589.5 | 56.4 | 711 | 8 | DR622988 | DR622988 | EST101311 |
| 43 | 589.5 | 56.4 | 770 | 8 | DR622508 | DR622508 | EST101263 |
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ALIGNMENTS

RESULT 1
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DEFINITION tricol3xe09.b1 T.reesei mycelial culture, Version 6 October 2003
ACCESSION CF867983
VERSION CF867983.1 GI:38122635
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Hypocrea jecorina
Rukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 744)
Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
14757250
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.
Location/Qualifiers
1. .744

JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

PUBMED 14757250

COMMENT

Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.
Location/Qualifiers
1. .744

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 /note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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 Percent Similarity: 95.16% Conservativeness: 4
 Best Local Similarity: 93.01% Mismatches: 8
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 DB: 7 Gaps: 0

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 Db 185 CAGACGATTTCAGCGCGGCACGGCTACAAACACGGCTACTTCTACTCGTACTGGAAACGAT 244
 Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 Db 245 GGCACCGCGCGGTGACGTACACCAATGCTCCCGCGGCGAGTTCTCCGTCAACTGGGTCC 304
 Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
 Db 305 AACTCGGCAACTTGTTCGGCGGCAAGGATGGCGAGCGCGGACCAACAGAGTCAATC 364
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 Qy 81 ArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 Db 425 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCCTACAAACCGTCCACG 484
 Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
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 Db 605 CGCCCAACACCACTCGGCGGCTCCGTCACACGCGGCAACCACTTCAACCGCGTGGGT 664
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 Qy 180 eSerSerGlySerAla 185
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RESULT 2
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 DEFINITION
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 CB898036
 ACCESSION
 CB898036.1 GI:30112694
 VERSION
 EST.
 SOURCE
 Hypocrea jecorina (anamorph: Trichoderma reesei)
 ORGANISM
 Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 1 (bases 1 to 799)
 Foreman, P.K., Brown, D.B., Dankmeyer, L., Dean, R., Diener, S.,
 Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,
 Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
 Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
 Transcriptional regulation of biomass-degrading enzymes in the
 filamentous fungus *Trichoderma reesei*
 J. Biol. Chem. 278 (34), 31988-31997 (2003)
 12788920
 Contact: Pamela K. Foreman
 Genencor Intl.
 925 Page Mill Road, Palo Alto, CA 94304, USA
 Tel: (650) 846-7635
 Fax: (650) 621-7817
 Email: Pforeman@genencor.com
 Seq primer: LT-F1 primer.
 Location/Qualifiers
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 /organism="Hypocrea jecorina"
 /mol_type="mRNA"
 /strain="QM6a"
 /db_xref="taxon:51453"
 /clone="tricolix09"
 /dev_stage="mycelia"
 /clone_lib="T. reesei mycelial culture, Version 3 april"
 /note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
 12788920

FEATURES
 source
 1..799

ORIGIN
 Alignment Scores:
 Pred. No.: 7,3e-95 Length: 799
 Score: 932.00 Matches: 173
 Percent Similarity: 95.16% Conservativeness: 4
 Best Local Similarity: 93.01% Mismatches: 8
 Query Match: 89.10% Indels: 1
 DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x CB898036 (1-799)
 Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
 Db 240 CAGACGATTTCAGCGCGGCACGGCTACAAACACGGCTACTTCTACTCGTACTGGAAACGAT 299
 Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
 Db 300 GGCACCGCGCGGTGACGTACCAATGCTCCCGCGGCGAGTTCTCCGTCACTGGTCC 359
 Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
 Db 360 AACTCGGCAACTTGTTCGGCGGCAAGGATGGCGAGCGCGGACCAACAGAGTCAATC 419
 Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
 Db 420 AACTTCTCGGCGAGCTACAAACCAACGCAACAGTACCTCTCCGTGTACGGTGGTCC 479
 Qy 81 ArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
 Db 480 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCCTACAAACCGTCCACG 539
 Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
 Db 540 GCGCCACCAAGCTGGCGAGGTCACTCCGACGCGGAGGTCTACGACATTTACCGCAGC 599
 Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
 Db 600 CAGCGCGTCAACACGCGTCCATCATCGGCACCGCACCTTTTACCGAGTACTGGTCCGTC 659
 Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
 Db 660 CGCCCAACCACTCGGCGGCTCCGTCACACGCGGCAACCACTTCAACCGCGTGGGT 719

```

Qy 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaVal-GluGlyTyrPhe 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 720 CAGCAAGGCGCTGACGCTCGGAGCAGTGGATTACCAAGATTGTTGCCGTGGAGGGTTACTT 779

Qy 180 eSerSerGlySerAla 185
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 780 TAGCTCTGGCTCTGCT 795

RESULT 3
CF881056 768 bp mRNA linear EST 31-OCT-2003
LOCUS trico83xj11.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone trico83xj11, mRNA sequence.
ACCESSION CF881056
VERSION CF881056.1 GI:38135738
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 768)
AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
TITLE Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL FEWS Microbiol. Lett. 230 (2), 275-282 (2004)
PUBMED 14757250
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: LT-F1 primer.
FEATURES
    source
        1..768
        /organism="Hypocrea jecorina"
        /mol_type="mRNA"
        /strain="QM6a"
        /db_xref="taxon:51453"
        /clone="trico83xj11"
        /dev_stage="mycelia"
        /clone_libs="T.reesei mycelial culture, Version 6 October
        2003"
        /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
        culture grown from 24 hrs to 6 days with varying Carbon
        and Nitrogen sources and concentrations."
ORIGIN
Alignment Scores:
Pred. No.: 1.19e-88 Length: 768
Score: 877.00 Matches: 167
Percent Similarity: 90.00% Conservative: 4
Best Local Similarity: 87.89% Mismatches: 19
Query Match: 83.84% Indels: 1
DB: 7 Gaps: 0

US-09-990-874B-55 (1-190) x CF881056 (1-768)

Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 189 CAGACGATTTCAGCCGGCAGCGGCTACACACGCGCTACTTCTACTCGTACTGGAACGAT 248

Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 249 GCGCACGCGCGGTGACGTACACCAATGCTCCGCGGCGGCGAGTTCTCCGTCACTGGTCC 308

Qy 41 AsnSerGlyAsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIle 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

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Db 309 AACTCGGCGCAACTTGTGCGCGGCAAGGATGGCAGCCGCGCACCAAGACAGGTCAATC 368
Qy 61 AenPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 369 AACTTCTCGGCGAGCTACACCCCAACGCGCAACAGTACTACTCTCCGTGTACGGTGGTCC 428

Qy 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 429 CGCAACCCCTGATCGAGTACTACATCGTTCGAGAATCTTGGCACCTACACCCGCTCCAGC 488

Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 489 GCGCGCACCAAGCTGGGCGAGTCACTCCGACGCGCTACGACATTTACCGCAGC 548

Qy 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 549 CAGCGGCTCAACACGCGCTCCATCATCGGCACCGNCACCTTTTACCAGTACTGGTCCGTTN 608

Qy 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 609 NCGCGCAACCAACCGCTCGAGCGGCTCGTCAAC-ACGGCGAACCACCTTCACACGCGTGGGCT 667

Qy 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 668 CAGCAAGGCGCTGACGCTCGNACGATGATACCCAGATGTTGCCGTGGAGGGTACTTNT 727

Qy 181 SerSerGlySerAlaSerIleThrValSer 190
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 728 AGCTCTGGCTCTGCTTCCATCACCCTGTCAGC 757

RESULT 4
CB907827 822 bp mRNA linear EST 02-JUL-2003
LOCUS trico83xj11 T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone trico83xj11, mRNA sequence.
ACCESSION CB907827
VERSION CB907827.1 GI:30122485
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 822)
AUTHORS Foreman,P.K., Brown,D.B., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
TITLE Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
JOURNAL J. Biol. Chem. 278 (34), 31988-31997 (2003)
PUBMED 12788920
COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
FEATURES
    source
        1..822
        /organism="Hypocrea jecorina"
        /mol_type="mRNA"
        /strain="QM6a"
        /db_xref="taxon:51453"
        /clone="trico83xj11"
        /dev_stage="mycelia"
        /clone_libs="T.reesei mycelial culture, Version 3 april"
        /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
        culture grown from 24 hrs to 6 days with varying Carbon
        and Nitrogen sources and concentrations."
ORIGIN
Alignment Scores:

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Pred. No.: 1.3e-88 Length: 822
Score: 877.00 Matches: 167
Percent Similarity: 90.00% Conservative: 4
Best Local Similarity: 87.89% Mismatches: 19
Query Match: 83.84% Indels: 1
DB: 6 Gaps: 0

US-09-990-874B-55 (1-190) x CB907827 (1-822)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 243 CAGACGATTCAGCCCGGACGGCTACACACACGGCTACTTCTACTCGTACTGGAAACGAT 302

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 303 GCCACACGGCGGTGACGTACACCAATGGTCCGGGGGCGAGTCTCCGTCACTGGTCC 362

QY 41 AsnSerGlyAsnPheValGlyGlyTyrGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 363 AACTCGGGCAACTTTGTTCGGCGCAAGGATGGCAGCCGCGGACCAAGGATCATC 422

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 423 AACTTCTCGGGCAGCTACAACCCCAACGCAACAGCTACCTCTCCGTGTACGGCTGGTCC 482

QY 81 ArgAsnProLeuIleGlnTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 483 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCAGCTACACCCGTCACG 542

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 543 GCGCCACCAAGCTGGCGGAGGTCACTCCGACGCGGAGGTCTACGACATTTACCGCAGC 602

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 603 CAGCGCGTCAACACGCGCTCATCATCGGCACCGNCACCTTNTACGAGTACTGGTCCGTTN 662

QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 663 NCGCCCAACCCCGCTCGACGGGGTCTGCTAC-ACGGGACACATTTACACGGTGGGCT 721

QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
DB 722 CAGCAAGCGCTGACGCTCGNAGCAGTGGATTACCCAGATGTTTGGCGTGAGGGTACTNT 781

QY 181 SerSerGlySerAlaSerIleThrValSer 190
DB 782 AGCTCTGGCTCTGCTTCCATCACCCTCAGC 811

RESULT 5
CD464145 738 bp mRNA linear EST 04-JUN-2003
LOCUS ETH1_48_B06.g1_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
DEFINITION clone ETH1_48_B06_A002 5', mRNA sequence.
ACCESSION CD464145
VERSION CD464145.1 GI:31385413
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 738)
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
Klein,R.R., Lian,C., Sun,F., Sullivan,R., Shah,M., Salzman,R.,
Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P.,
Olaseinde,O., Eastman,A. and Pratt,L.H.
An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
(ACC)-treated seedlings
Unpublished (2003)
Other ESTs: ETH1_48_B06.b1_A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
```

The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).

Location/Qualifiers

1..738

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="BTx623"

/db_xref="taxon:4558"

/clone="ETH1_48_B06_A002"

/lab_host="DH10B-T1 phage-resistant E. coli"

/clone_lib="Ethylene-treated seedlings"

/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
material from both time points was combined prior to RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites of the
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."

ORIGIN

Alignment Scores:

Pred. No.: 2.11e-66 Length: 738

Score: 680.50 Matches: 126

Percent Similarity: 77.96% Conservative: 19

Best Local Similarity: 67.74% Mismatches: 40

Query Match: 65.06% Indels: 1

DB: 6 Gaps: 1

US-09-990-874B-55 (1-190) x CD464145 (1-738)

QY 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23

DB 182 CAGCCCACTACTGGCTCAAGCGGTGGCTACTACTTCTCTTCTGGACTGATACACCCCAAC 241

QY 24 GlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGly 43

DB 242 TCTGTCACTTACACCAACGCGGACCGTGGCCAGTTCAGCTGACGTGGAATGGAACCGT 301

QY 44 AsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSer 63

DB 302 AACCAAGTCTGGTGAAGGGCTGGATGCCGCTGGTGTCT---CGCACCATCAAGTACTCT 358

QY 64 GlySerTyrAsnProAsnGlyAsnSerTyrIleuAlaValTyrGlyTrpSerArgAsnPro 83

DB 359 GGTACTTACAACATCAACCGAAACAGCTACCTCGCTGTTTACGGATGGACTCAGAACCCCT 418

QY 84 LeuIleGlyTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103

DB 419 CTCATCGAGTACTACATCGTTGAGAACTTCGCGCACTCAACCCCTCTTCCGGCGGCCAG 478

QY 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123

DB 479 AAGAGGGTGAAGTCACTGTTGACGGATCTCTACGACATCTACGTGACGACCCGCTGTC 538

QY 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsn 143


```

/db_xref="taxon:117187"
/clone="FVNCX47"
/tissue_type="mycelia"
/clone_lib="FvM"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
and a 72 hour, liquid GYM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (CDNA Synthesis Kit; Stratagene)."
```

ORIGIN

| | | | |
|------------------------|----------|---------------|-----|
| Alignment Scores: | | | |
| Pred. No.: | 8.39e-64 | Length: | 883 |
| Score: | 558.50 | Matches: | 116 |
| Percent Similarity: | 78.26% | Conservative: | 28 |
| Best Local Similarity: | 63.04% | Mismatches: | 39 |
| Query Match: | 62.95% | Indels: | 1 |
| DB: | 8 | Gaps: | 1 |

US-09-990-874B-55 (1-190) x DR643230 (1-883)

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QY      7  ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTTPAsnAspGlyHisGlyValThr 26
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     136  TCGGTACTAACACGGATTCTTCTACTCTGTGTGATGATGCGGTCCGATCGTACT 195

QY      27  MetThrLeuGlyProGlyGlyGlnPheSerValAsnTTPSerAsnSerGlyAsnPheVal 46
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     196  TACACCAACGGTGGAGGAGGTCTTACTCCATGGAGTGGAGGATGGTGGTAACCTCGTC 255

QY      47  GlyGlyValGlyTTPGlnProGlyThrIysAsnIysValIleAsnPheserGlySerTyr 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     256  GGTGGTAAGGGTGGTCTCTCTCGGA---AAAGCTCGAACCACTCTCTATGAGGAGGATAC 312

QY      67  AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTTPSerArgAsnProLeuIleGlu 86
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     313  AAGCCCAAGGCAACAGACTACTCTCCGTCTACGGCTGGACCCGAAACCCCTAGTCGAG 372

QY      87  TyrTyrIleValGluAsnPhGlyThrTyrAsnProSerThrGlyAlaThrIysHisGly 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     373  TACTACATCGTAGAGTCTCTCGGTACCTACACCCCTCCAGCGGTGCTACCAAGAAGGGT 432

QY     107  GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     433  ACCGTTGAGGCTGATGGCAGCACCTACACACTTTTCGAGACTTTCGCACCAACGCCCT 492

QY     127  SerIleGluGlyThrAlaThrPheTyrGlnTyrTTPSerValArgAsnArgArgSer 146
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     493  TCATCCAGCGTACTCAGACCTTCCAGCAGTACTGTGTCTGTTCGCAGCAGCATCGCTCT 552

QY     147  SerGlySerValAsnThrAlaAsnHisPheAsnAlaTTPAlaArgGlnGlyLeuThrIleu 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     553  ACTGGTAGCGTTGACACTGGTCTTCACTTCGACGCTGGAGAAAGCGTGGTATGAAGCTC 612

QY     167  GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     613  GGTACCCACGACTACCATCTCGCTACTAGGGGTACTTTCAGCAGCGGATCTTCTTCAC 672

QY     187  IleThrValSer 190
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     673  ATGACCGGTTCT 684
```

RESULT 8
DR707969
LOCUS
DEFINITION
Asn_08783 Aspergillus niger pbluescript (EcoRI-XhoI) Aspergillus
niger cDNA clone Asn_08783, mRNA sequence.
DR707969
ACCESSION
VERSION
DR707969.1 GI:70824260

```

Db      367  TCCATTGAGGACCGCTACCTTCACTCAGTACTGGTCCGTTGCGCAGAACAGAGAGTT 426
      |||.....|
Qy      147  SerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeu 166
      |||.....|
Db      427  GCGGGAACCGTTACCACTCCCAACACACTCAATGCTGGGCTTAAGCTGGGAATGAACCTG 486
      |||.....|
Qy      167  GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
      |||.....|
Db      487  GGTACTCAACTACCAAGATCGTGCTACCGAGGGTTACCAAGAGCGTGGATCTTCGTCC 546
      |||.....|
Qy      187  IleThrVal 189
      |||.....|
Db      547  ATCACTGTT 555

```

```

RESULT 9
DR701170 746 bp mRNA linear EST 14-JUL-2005
LOCUS Asn_00615 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus
DEFINITION niger cDNA clone Asn_00615, mRNA sequence.
ACCESSION DR701170
VERSION DR701170.1 GI:70817461
KEYWORDS EST.
SOURCE Aspergillus niger
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 746)
Tsang,A., Storms,R. and Bulter,G.
Expressed sequence tags from Aspergillus niger cDNA library
Unpublished (2005)
Contact: Tsang A
Centre for Structural and Functional Genomics
Concordia University
7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
POLYA=No.
Location/Qualifiers
1..746
/organism="Aspergillus niger"
/mol_type="mRNA"
/strain="N402"
/db_xref="taxon:5061"
/clone="Asn_00615"
/dev_stage="mycelial growth"
/lab_host="E. coli"
/clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
EcoRI; Vector: pBluescript KS+; Site 1: XhoI; Site 2:
(Stratagene) using poly(A)+RNA isolated from Aspergillus
niger cultured under different carbon sources (glucose,
maltose, xylose, lactose, sorbitol, xylan, and bran).
Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
adaptors were ligated to the blunt-ended, double-stranded
cDNA. The EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp).

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FEATURES

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source
1..746
/organism="Aspergillus niger"
/mol_type="mRNA"
/strain="N402"
/db_xref="taxon:5061"
/clone="Asn_00615"
/dev_stage="mycelial growth"
/lab_host="E. coli"
/clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
EcoRI; Vector: pBluescript KS+; Site 1: XhoI; Site 2:
(Stratagene) using poly(A)+RNA isolated from Aspergillus
niger cultured under different carbon sources (glucose,
maltose, xylose, lactose, sorbitol, xylan, and bran).
Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
adaptors were ligated to the blunt-ended, double-stranded
cDNA. The EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp).

```

ORIGIN

```

Alignment Scores:
Pred. No.: 7,34e-62 Length: 746
Score: 640.50 Matches: 115
Percent Similarity: 77.60% Conservative: 27
Best Local Similarity: 62.84% Mismatches: 40
Query Match: 61.23% Indels: 1
DB: 8 Gaps: 1

```

US-09-990-874b-55 (1-190) x DR701170 (1-746)

```

Qy      7  ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
      |||.....|
Db      149  ACCGGGAGAACACCGGCTTCTACTACTCTTCTGACCGCGGTGGAGAGCGTGACC 208

```

```

Qy      27  MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
      |||.....|
Db      209  TACACCAACGAGAGATGCTGGTGCCTCACACTGTTGAGTGGTCCAACTGGGCACTTTGTC 268
      |||.....|
Qy      47  GlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyr 66
      |||.....|
Db      269  GGTGGAAAGGGCTGGAAACCCCGGAAGTCCGCAGAC---ATCACCTACAGCGGCACCTTC 325
      |||.....|
Qy      67  AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrPheSerArgAsnProLeuIleGlu 86
      |||.....|
Db      326  ACCCTAGCGGCAACGGCTACCTCTCGTCTATGCTGGACCACTGACCCCTCTGATCGAG 385
      |||.....|
Qy      87  TyrTrileValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGly 106
      |||.....|
Db      386  TACTACATCGTGGAGTCTACCGCGACTACCAACCCCGCGCAGTGGAGGCGCAGTACAGGCG 445
      |||.....|
Qy      107  GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
      |||.....|
Db      446  ACCGTCACTCCGAGCGGATCCGTTACGATATCTACACGGGTACCCGTACCCATGCTGCT 505
      |||.....|
Qy      127  SerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSer 146
      |||.....|
Db      506  TCCATTAGGGAACCGGTACCTTCACTCAGTACTGGTCCGTTGCGCAGACCAAGAGAGTT 565
      |||.....|
Qy      147  SerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeu 166
      |||.....|
Db      566  GCGGGAACCGTTACCACTCCCAACCACTTCAATGCTGGGCTAAGCTGGGAATGAACCTG 625
      |||.....|
Qy      167  GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
      |||.....|
Db      626  GGTACTCACACTACCAAGATCGTGCTACCGAGGGTTACCAAGAGCGTGGATCTTCGTCC 685
      |||.....|
Qy      187  IleThrVal 189
      |||.....|
Db      686  ATCACTGTT 694

```

RESULT 10

```

CB901964 746 bp mRNA linear EST 02-JUL-2003
LOCUS trico28x108 T. reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone trico28x108, mRNA sequence.
ACCESSION CB901964
VERSION CB901964.1 GI:30116622
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 746)
Foreman,P.K., Brown,D.B., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
12788920
PUBMED
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1..746
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="trico28x108"
/dev_stage="mycelia"

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FEATURES

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source
1..746
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="trico28x108"
/dev_stage="mycelia"

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/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

Alignment Scores: 1.41e-61 Length: 746
Pred. No.: 638.00 Matches: 122
Score: 82.24% Conservative: 3
Percent Similarity: 80.26% Mismatches: 27
Best Local Similarity: 60.99% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-09-990-874B-55 (1-190) x CB901964 (1-746)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAep 20
|||||
DB 291 CAGACGANNACGCCGGCAGCGGCTACACACCCGCTACNNCTACTCGNACCGGAACGAN 350

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
|||||
DB 351 GGCCAAAAGCGGACGACGACCAAGGNGCCCGCGGCGAGNCTTCGCCCAACCGGGGCC 410

QY 41 AenSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
|||||
DB 411 AACNCGGGCAACNNGCGCGGCGGAGGAGGCGGAGCGGCGGACCAAGACGAGGCGCAC 470

QY 61 AenPheSerGlySerTyrAsnProAenGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
|||||
DB 471 AACTTCTCGGCGAGCTACACCCCAACGCAACAGCTACCTCTCGGTGTACGGGTGGTCC 530

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
|||||
DB 531 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACTTACCAACCCGTCACG 590

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
|||||
DB 591 GGCGCCACCAAGCTGGCGAGGTCACTCCGACGGGAGGCTACGACATTTACCGCAGC 650

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
|||||
DB 651 CAGCGCGTCAACAGCGGTCCATCATCGGCACCGCCACCTTTTACGAGTACTGGTCCGTC 710

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThr 152
|||||
DB 711 CGCGCACCCACCGCTCGAGCGGGTCCGTCACACG 746

RESULT 11

CF871731
LOCUS trico28xi08.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone trico28xi08, mRNA sequence.

ACCESSION CF871731

VERSION CF871731.1 GI:38126413

KEYWORDS

SOURCE EST.

ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)

Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 746)

Dienes, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,

Tennis, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,

Ward, M., and Dean, R.A.

Characterization of the protein processing and secretion pathways

in a comprehensive set of expressed sequence tags from Trichoderma

reesei

FEWS Microbiol. Lett. 230 (2), 275-282 (2004)

14757250

Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: ralph.dean@ncsu.edu

Seq primer: Tr-F1 primer.

Location/Qualifiers

source

1.746
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clones="trico28xi08"
/dev_stages="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

Alignment Scores: 1.41e-61 Length: 746
Pred. No.: 638.00 Matches: 122
Score: 82.24% Conservative: 3
Percent Similarity: 80.26% Mismatches: 27
Best Local Similarity: 60.99% Indels: 0
Query Match: 7 Gaps: 0
DB:

US-09-990-874B-55 (1-190) x CF871731 (1-746)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAep 20
|||||
DB 291 CAGACGANNACGCCGGCAGCGGCTACACACCCGCTACNNCTACTCGNACCGGAACGAN 350

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
|||||
DB 351 GGCCAAAAGCGGACGACGACCAAGGNGCCCGCGGCGAGNCTTCGCCCAACCGGGGCC 410

QY 41 AenSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
|||||
DB 411 AACNCGGGCAACNNGCGCGGCGGAGGAGGCGGAGCGGCGGACCAAGACGAGGCGCAC 470

QY 61 AenPheSerGlySerTyrAsnProAenGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
|||||
DB 471 AACTTCTCGGCGAGCTACACCCCAACGCAACAGCTACCTCTCGGTGTACGGGTGGTCC 530

QY 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
|||||
DB 531 CGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACTTACCAACCCGTCACG 590

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
|||||
DB 591 GGCGCCACCAAGCTGGCGAGGTCACTCCGACGGGAGGCTACGACATTTACCGCAGC 650

QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
|||||
DB 651 CAGCGCGTCAACAGCGGTCCATCATCGGCACCGCCACCTTTTACGAGTACTGGTCCGTC 710

QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThr 152
|||||
DB 711 CGCGCACCCACCGCTCGAGCGGGTCCGTCACACG 746

RESULT 12

DR705641

LOCUS

DEFINITION

Asn_05863 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus

niger cDNA clone Asn_05863, mRNA sequence.

ACCESSION DR705641

VERSION DR705641.1

KEYWORDS

SOURCE

ORGANISM

Aspergillus niger

Aspergillus niger

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

664 bp mRNA linear EST 14-JUL-2005

Asn_05863 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus

niger cDNA clone Asn_05863, mRNA sequence.

ACCESSION DR705641

VERSION DR705641.1

KEYWORDS

SOURCE

Aspergillus niger

Aspergillus niger

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

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REFERENCE 1 (bases 1 to 664)
AUTHORS Tsang,A., Storms,R. and Bulter,G.
TITLE Expressed sequence tags from Aspergillus niger cDNA library
JOURNAL Unpublished (2005)
COMMENT Contact: Tsang A
Centre for Structural and Functional Genomics
Concordia University
7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
POLYA=No. Location/Qualifiers
          1..664
          /organism="Aspergillus niger"
          /mol_type="mRNA"
          /strain="N402"
          /db_xref="taxon:5061"
          /dev_stage="mycelial growth"
          /lab_host="E. coli"
          /clone="Asn_05863"
          /clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
          /note="Vector: pBluescript KS+; Site 1: XhoI; Site 2:
          EcoRI; Complementary DNA was synthesized with ZAP Kit
          (Stratagene) using poly(A)+RNA isolated from Aspergillus
          niger cultured under different carbon sources (glucose,
          maltose, xylose, lactose, sorbitol, xylan, and bran).
          Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
          adaptors were ligated to the blunt-ended, double-stranded
          cDNA. The EcoRI-XhoI-digested cDNA was ligated with
          EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp)."

FEATURES
    source
    Alignment Scores:
    Pred. No.: 1..116-60 Length: 664
    Score: 629.50 Matches: 113
    Percent Similarity: 77.53% Conservative: 25
    Best Local Similarity: 63.48% Mismatches: 39
    Query Match: 60.18% Indels: 1
    DB: 8 Gaps: 1

US-09-990-874B-55 (1-190) x DR705641 (1-664)

QY 12 GlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThrMetThrLeuGlyPro 31
DB 3 GCTTCTACTACTCTTCTGGACCGACGGGTGGAGAGCTGCTACCTACCAACGGAGAT 62
QY 32 GlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheValGlyGlyTyr 51
DB 63 GCTGGTGCCTACACTGTTGAGTGTGTCACACGTGGGCACTTGTGCGTGAAGGCTGG 122
QY 52 GlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnGly 71
DB 123 AACCCCGGAAGTGGCGAGGAC---ATCCACTACAGCGGCACCTTCAACCCCTAGCGGAC 179
QY 72 SerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeuIleGluTyrTyrIleValGlu 91
DB 180 GGCTACCTTCCTCGTATGGCTGGACCTGACCTGACCTCTGATCGAGTACTACATGTCGAG 239
QY 92 AsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSerAsp 111
DB 240 TCCTACGGCGACTACACCCCGGAGTGGAGCGACGCTACAGGCGACCGTCACTCGGAC 299
QY 112 GlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluGlyThr 131
DB 300 GGATCCGTTTACGATATCTACACGGCTACCCGCTACCAATGCTGCTTCCATTCCAGGGAAC 359
QY 132 AlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerSerGlySerValAsn 151
DB 360 GCTACCTTCCTACGTAAGTGGTTCGCTCCGAGAACAGAGAGATGGCGGGAACCGTTACC 419
QY 152 ThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyr 171

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Db 420 ACCTCAACCACTTCATGCTTGGGCTAAGCTGGGAATGAACCTGGTACTCACAACACTAC 479
QY 172 GlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
Db 480 CAGATCGTGGCTACCGAGGGTTACCGAGACGTCGTGATCTTCGTCATCACTGTT 533

RESULT 13
DR702584 682 bp mRNA linear EST 14-JUL-2005
LOCUS Asn_02201 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus
DEFINITION niger cDNA clone Asn_02201, mRNA sequence.
ACCESSION DR702584
VERSION DR702584
KEYWORDS DR702584.1 GI:70818875
SOURCE Aspergillus niger
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 682)
AUTHORS Tsang,A., Storms,R. and Bulter,G.
TITLE Expressed sequence tags from Aspergillus niger cDNA library
JOURNAL Unpublished (2005)
COMMENT Contact: Tsang A
Centre for Structural and Functional Genomics
Concordia University
7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
POLYA=No. Location/Qualifiers
          1..682
          /organism="Aspergillus niger"
          /mol_type="mRNA"
          /strain="N402"
          /db_xref="taxon:5061"
          /clone="Asn_02201"
          /dev_stage="mycelial growth"
          /lab_host="E. coli"
          /clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
          /note="Vector: pBluescript KS+; Site 1: XhoI; Site 2:
          EcoRI; Complementary DNA was synthesized with ZAP Kit
          (Stratagene) using poly(A)+RNA isolated from Aspergillus
          niger cultured under different carbon sources (glucose,
          maltose, xylose, lactose, sorbitol, xylan, and bran).
          Synthesis was primed with oligo(dT)/XhoI primer. EcoRI
          adaptors were ligated to the blunt-ended, double-stranded
          cDNA. The EcoRI-XhoI-digested cDNA was ligated with
          EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp)."

ORIGIN
    Alignment Scores:
    Pred. No.: 5..496-60 Length: 682
    Score: 623.50 Matches: 111
    Percent Similarity: 77.09% Conservative: 27
    Best Local Similarity: 62.01% Mismatches: 40
    Query Match: 59.61% Indels: 1
    DB: 8 Gaps: 1

US-09-990-874B-55 (1-190) x DR702584 (1-682)

QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
DB 149 ACCGGCGAGAACACCGGCTTCTACTCTCTGGACGACGGGGTGGAGACGTGACC 208
QY 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
DB 209 TACACCAACGAGATGCTGCTGCTACACTGTTGAGTGTGCTCCACGTGGCACTTTGTC 268
QY 47 GlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyr 66
DB 269 GGTGGAAGGGCTGGAACCCCGGAAGTGGCAGGAC---ATCACCTACAGCGCACCTTC 325

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QY 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeuLeuGlu 86
Db 326 ACCCTTAGCGGCAACGGCTACCTCTCGTCTATGGTGGACCACTGACCTCTGATCGAG 385
QY 87 TyrTyrIleValGluAsnPhedGlyThrTyrAsnProSerThrGlyAlaThrIysHisGly 106
Db 386 TACTATCATGTCGAGTCTTACGCGCAGTCAACACCGCGGAGTGAGGCGACGTACAAGGCG 445
QY 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
Db 446 ACCGTCACTCGAGCGATCCGCTTACGATATCTACACGCTACCGCTACCATGCTGTCT 505
QY 127 SerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsnArgSer 146
Db 506 TCAATTCAGGGAACCGCTACCTTCACTCACTAGTACTGCTCGCTCGCCAGAACAGAGATT 565
QY 147 SerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeuThrLeu 166
Db 566 GCGGGAACCGTTACCACTCCCAACCACTTCAATGCTTGGCTTAAGTGGGAATGAACCTG 625
QY 167 GlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAla 185
Db 626 GGTACTCAACAATACCAATACCATGCTGGCTACGAGGGTTACAGAGCACTGATCTTCG 682

RESULT 14
A0160254/c
LOCUS
DEFINITION
750 bp DNA linear GSS 09-SEP-1998
mgx0003L119: CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgx0003L119, genomic survey sequence.
A0160254
A0160254.1 GI:3557243
GSS.
Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 750)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 344.
Location/Qualifiers
1. .750
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgx0003L119"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/notes="Vector: pBACWICH; Site 1: HindIII, Site 2: HindIII,
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

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ORIGIN
Alignment Scores:
Pred. No.: 7,12e-60 Length: 750
Score: 623.00 Matches: 120
Percent Similarity: 67.14% Conservative: 23
Best Local Similarity: 56.34% Mismatches: 39
Query Match: 59.56% Indels: 31
DB: 9 Gaps: 3
US-09-990-874B-55 (1-190) x A0160254 (1-750)
QY 8 GlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGly---ValThr 26
Db 640 GGGAAACCAACAAACGGTTTTTACTACTCCCACTGGACCGCAATGCGCGGCGACACGTGCACN 581
QY 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
Db 580 TACACATGAGCGGAGCGTGGTTCAGTTTTCGTACAGTGGCGGACCCAGCGGCACTTTGTTC 521
QY 47 GlyGlyLysGlyTyrGlnProGlyThr----- 55
Db 520 GGTGGAAAGGTTGGAAACCGGCAATGCTGGTGAGTTTTTTGTTTGTCTTTTGTCTCA 461
QY 56 -----Lys-AsnLys 58
Db 460 TGTACTTTTCCCAAAAAAGGAAAAAAGAGACTAACCAACAACAACAAAAACAGCCG 401
QY 58 sValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGln 78
Db 400 CGTCATCAACTACTCGGGAGCTACAGCCNCGAGGCACTCATCTACCTGGCCGCTACCGG 341
QY 78 YTrpSerArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnPr 98
Db 340 CTGGAGCGGCAACCGCTGATCGTACTACGTGGTGAGAGCTTTGGCAGCTACAACCC 281
QY 98 oSerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCy 118
Db 280 GTCTGTCGGCGGCCAACCAACCGCGGCTCTTCACTCGGACGCGCAGCACCTACGACATCT 221
QY 118 sArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTr 138
Db 220 GGTACGACCCCTCATACACCGCTTCATCGGCGCACCAAGACCTTTTCAGCAGTCTCTG 161
QY 138 pSerValArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAl 158
Db 160 GTCTGTCGGCGGCCAACAGCGGCCAGCGCACCTTTGGCAACCAACCGTCAACGC 101
QY 158 aTrpAlaArgGlnGlyLeuThrLeuGlyThrMet---AspTyrGlnIleValAlaValGln 177
Db 100 CTGGCGCAACGCGCGCTCAACCTCGGCAACAGTGGAACTACCAATCTCTGGCCGCTCGA 41
QY 177 uGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
Db 40 GGGCTACACACAGCGCGCTCCGCCAGCATGACTGTC 4

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RESULT 15
CV496238
LOCUS
DEFINITION
73987.1 Cold Sweetening B Solanum tuberosum cDNA clone 73987 5',
mRNA sequence.
CV496238
CV496238.1 GI:53778595
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 712)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Laque, M., De
Koeyer, D., Aude, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
Generation of ESTs from tubers following 3 months storage at 4

```

degrees celsius, and 95% relative humidity
Unpublished (2004)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..712
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="73987"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Cold Sweetening B"
/note="Vector: pBluescript II SK(+). XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Developmental series. Plants from
pathogen-free Solanum tuberosum var. Shepody, clone 1756,
nuclear stock were grown in a greenhouse under natural
conditions. Mature, harvested tubers were stored in the
dark at 4C, 95% relative humidity for 3 months. RNA was
isolated for library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Alignment Scores:

Pred. No.: 7,566-60 Length: 712
Score: 622.50 Matches: 119
Percent Similarity: 79.03% Conservative: 28
Best local Similarity: 63.98% Mismatches: 35
Query Match: 59.51% Indels: 4
DB: 7 Gaps: 3

US-09-990-874B-55 (1-190) x CV496238 (1-712)

| | | | |
|----|-----|--|-----|
| Qy | 7 | ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThr | 26 |
| Db | 61 | ACCGGTACTAGTGGTGGTTACTACTCTCTGGACCGGTAAGCGGTGGTTACTA | 120 |
| Qy | 27 | MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer---AsnSerGlyAsnPhe | 45 |
| Db | 121 | TACTCCACGGAGCCAAATGGTCATATATGCGTAGCTGGACCGGTAAAGGGTAACCTTC | 180 |
| Qy | 46 | ValGlyGlyLeGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSerGlySer | 65 |
| Db | 181 | GTCCGTGGAAAGGATGGGCTGTTGGTCCGAG---CGCTCCATCTCTTACACCGGATCC | 237 |
| Qy | 66 | TyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIle | 85 |
| Db | 238 | TACAAACCCACGGAACCTCTACCTCTCCGTCTATGGTGGACTACCTCCCCCTCATC | 297 |
| Qy | 86 | GluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHis | 105 |
| Db | 298 | GAATACTACTCTGTCGAAGACCTTTGGACCTAGGATCCCTCTCCGCCGCCACCGAATC | 357 |
| Qy | 106 | GlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAla | 125 |
| Db | 358 | GGCAGTGTCACCTCCGACGGTTCACATACAAGATCCTCGAGACCACCGGTACAAACCAA | 417 |
| Qy | 126 | ProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgArg | 145 |
| Db | 418 | CCTTCGTTCAAGGAACCTGCTACTCTCAAGCAATACTGGTCCGTCCGTACTAGCAAGCGT | 477 |
| Qy | 146 | SerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThr | 165 |
| Db | 478 | ACGAGCGGTACCGTACCACTGCAAAACCAATTTGCAGCCTGGAGAGTTGGATTGACT | 537 |
| Qy | 166 | LeuGly---ThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer-SerGlySe | 184 |
| Db | 538 | TTGGGCTCAAGCTACAAAGTACCAATTTGCTGTTGAGGGGTACCAAGCAAGTGGTTC | 597 |

Qy 184 rAlaSerIleThrVal 189
Db 598 CGATTCCATCACTGTT 613

Search completed: December 30, 2005, 03:32:44
Job time : 3759 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 01:16:22 ; Search time 165 Seconds
(without alignments)
2046.889 Million cell updates/sec

Title: US-09-990-874B-55
Perfect score: 1046
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPOP=7 -YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 948 | 90.6 | 573 | 2 | US-08-709-912-18 |
| 2 | 948 | 90.6 | 573 | 2 | US-09-047-370-18 |
| 3 | 946 | 90.4 | 1015 | 2 | US-08-121-436A-1 |
| 4 | 939 | 87.9 | 822 | 3 | US-09-254-733-8 |
| 5 | 687 | 65.7 | 1281 | 3 | US-08-768-373-1 |
| 6 | 687 | 65.7 | 1281 | 3 | US-09-849-242A-1 |
| 7 | 643.5 | 61.5 | 983 | 2 | US-08-886-765-1 |
| 8 | 643.5 | 61.5 | 983 | 3 | US-09-115-660-1 |
| 9 | 635 | 60.7 | 1174 | 3 | US-08-768-373-3 |

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| 10 | 635 | 60.7 | 1174 | 3 | US-09-849-242A-3 | Sequence 3, Appli |
| 11 | 629.5 | 60.2 | 1219 | 2 | US-08-230-979A-7 | Sequence 7, Appli |
| 12 | 611.5 | 58.5 | 1375 | 3 | US-08-468-812-1 | Sequence 1, Appli |
| 13 | 611.5 | 58.5 | 1375 | 3 | US-08-590-563-1 | Sequence 1, Appli |
| 14 | 611.5 | 58.5 | 1375 | 3 | US-09-770-621-1 | Sequence 1, Appli |
| 15 | 611.5 | 58.5 | 1375 | 3 | US-09-235-832-1 | Sequence 1, Appli |
| 16 | 609 | 58.2 | 927 | 2 | US-08-507-431-5 | Sequence 5, Appli |
| 17 | 609 | 58.2 | 927 | 2 | US-08-902-655A-5 | Sequence 5, Appli |
| 18 | 609 | 58.2 | 927 | 3 | US-09-116-622-5 | Sequence 5, Appli |
| 19 | 609 | 58.2 | 927 | 3 | US-09-219-277-5 | Sequence 5, Appli |
| 20 | 609 | 58.2 | 927 | 3 | US-09-599-661-5 | Sequence 5, Appli |
| 21 | 605.5 | 57.9 | 2898 | 3 | US-09-462-246-1 | Sequence 1, Appli |
| 22 | 602.5 | 57.6 | 1123 | 2 | US-08-458-023B-3 | Sequence 3, Appli |
| 23 | 601.5 | 57.3 | 2055 | 3 | US-08-367-891A-1 | Sequence 1, Appli |
| 24 | 557 | 53.3 | 675 | 2 | US-07-744-570B-1 | Sequence 1, Appli |
| 25 | 537.5 | 51.4 | 847 | 3 | US-09-260-283-1 | Sequence 1, Appli |
| 26 | 537.5 | 51.4 | 1244 | 3 | US-08-591-685-12 | Sequence 12, Appli |
| 27 | 525.5 | 50.2 | 1207 | 2 | US-08-575-964-2 | Sequence 2, Appli |
| 28 | 525.5 | 50.2 | 1207 | 2 | US-08-963-500-2 | Sequence 2, Appli |
| 29 | 521 | 49.8 | 744 | 3 | US-09-189-060B-1 | Sequence 1, Appli |
| 30 | 501.5 | 47.9 | 642 | 2 | US-08-104-445-2 | Sequence 2, Appli |
| 31 | 501.5 | 47.9 | 1413 | 2 | US-08-104-445-1 | Sequence 1, Appli |
| 32 | 497 | 47.5 | 720 | 2 | US-08-044-621D-1 | Sequence 1, Appli |
| 33 | 496 | 47.4 | 572 | 2 | US-08-044-621D-2 | Sequence 2, Appli |
| 34 | 496 | 47.4 | 572 | 2 | US-08-044-621D-3 | Sequence 3, Appli |
| 35 | 496 | 47.4 | 579 | 2 | US-08-709-912-19 | Sequence 19, Appli |
| 36 | 496 | 47.4 | 579 | 2 | US-09-047-370-19 | Sequence 19, Appli |
| 37 | 496 | 47.4 | 1349 | 3 | US-09-570-856B-2 | Sequence 2, Appli |
| 38 | 489 | 46.7 | 663 | 3 | US-08-470-953A-1 | Sequence 1, Appli |
| 39 | 489 | 46.7 | 663 | 3 | US-08-470-953A-2 | Sequence 2, Appli |
| 40 | 489 | 46.7 | 744 | 3 | US-09-189-060B-1 | Sequence 1, Appli |
| 41 | 489 | 46.7 | 744 | 3 | US-08-470-953A-4 | Sequence 4, Appli |
| 42 | 489 | 46.7 | 744 | 3 | US-08-470-953A-5 | Sequence 5, Appli |
| 43 | 489 | 46.7 | 871 | 2 | US-08-698-978-1 | Sequence 1, Appli |
| 44 | 489 | 46.7 | 1513 | 3 | US-08-470-953A-10 | Sequence 10, Appli |
| 45 | 489 | 46.7 | 1513 | 3 | US-08-470-953A-11 | Sequence 11, Appli |

ALIGNMENTS

RESULT 1
US-08-709-912-18
; Sequence 18, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr. Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pTVX(3-190)
US-08-709-912-18

Alignment Scores:
Pred. No.: 2,448-98 Length: 573
Score: 948.00 Matches: 174
Percent Similarity: 95.24% Conservative: 6
Best Local Similarity: 92.06% Mismatches: 9
Query Match: 90.63% Indels: 0
DB: 2 Gaps: 0

US-09-990-874B-55 (1-190) x US-08-709-912-18 (1-573)

QY 2 ThrileGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 3 AGCATAGGACCCAGGACCGGTTTCAACACCGGTACTTTTACAGCTATTGGACGATGCG 62
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
DB 63 CATGGTGGTGTACCTATACAAACGCGCGGAGGCCAATTTAGCGTCAATGGTCTAAC 122
QY 42 SerGlyAsnPhaValGlyGlyTyrGlnProGlyThrLysAsnLysValIleAsn 61
DB 123 TCCGGAATCTCGTAGGTGGAAGGTTGCAACCGCGGACCAAAATAAGGTGATCAAC 182
QY 62 PheSerGlySerTyrAsnProGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 183 TTCTCTGGATCTTATTAATCCGATGGGAATTCATCTTAAGCGTCTATGGCTGGTCTAGA 242
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPhaGlyThrTyrAsnProSerThrGly 101
DB 243 AACCCACTGATTGAATATTACATTGTGGAATTTCCGTTACCTACCAATCCGAGTACCGGC 302
QY 102 AlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspIleCysArgThrGln 121
DB 303 GCCACAAATTAAGCGGAGTCACTAGTAGTATCGGTATATGATATCTACCGTACCCAA 362
QY 122 ArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArg 141
DB 363 CCGGTTAATCAGCCATCGATCATTTGAACCGCCACCTTTTATCAGTACTGGAGTGTAGA 422
QY 142 ArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArg 161
DB 423 CGTACCGCATCGAGCTCCGGTTCGTTAATCTCGAATCACTTATGATCGATGGGACAG 482
QY 162 GlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSer 181
DB 483 CAAGGGTTAACCTAGGTACATGGATTATCAATCGTAGCGGTGGAAGGCTACTTCTCG 542
QY 182 SerGlySerAlaSerIleThrValSer 190
DB 543 AGTGGTTCCGCTAGTATTACAGTGAGC 569

RESULT 2

US-09-047-370-18
Sequence 18, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto

APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pTVX(3-190)
US-09-047-370-18

Alignment Scores:
Pred. No.: 2,448-98 Length: 573
Score: 948.00 Matches: 174
Percent Similarity: 95.24% Conservative: 6
Best Local Similarity: 92.06% Mismatches: 9
Query Match: 90.63% Indels: 0
DB: 2 Gaps: 0

US-09-990-874B-55 (1-190) x US-09-047-370-18 (1-573)

QY 2 ThrileGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 3 AGCATAGGACCCAGGACCGGTTTCAACACCGGTACTTTTACAGCTATTGGACGATGCG 62
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
DB 63 CATGGTGGTGTACCTATACAAACGCGCGGAGGCCAATTTAGCGTCAATGGTCTAAC 122
QY 42 SerGlyAsnPhaValGlyGlyTyrGlnProGlyThrLysAsnLysValIleAsn 61
DB 123 TCCGGAATCTCGTAGGTGGAAGGTTGCAACCGCGGACCAAAATAAGGTGATCAAC 182
QY 62 PheSerGlySerTyrAsnProGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 183 TTCTCTGGATCTTATTAATCCGATGGGAATTCATCTTAAGCGTCTATGGCTGGTCTAGA 242
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPhaGlyThrTyrAsnProSerThrGly 101

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|-----|----|-----|-----|------------|------|-------|------|-----|------|------|---------|---------|-----------|-----|-----|
| 243 | Db | A | ACC | CACTGATTGA | ATAT | TACAT | TTCG | GA | AAAT | TTCG | TACCTAC | CAATCCG | AGTACCGGC | 302 | |
| 102 | Qy | A | Ala | Thr | Iys | H | S | G | I | G | L | u | Val | Thr | Ser |
| 303 | Db | G | C | C | A | A | A | A | A | T | T | A | G | C | A |
| 122 | Qy | A | Arg | Val | Asn | Ala | Pro | Ser | I | e | L | u | G | L | Y |
| 363 | Db | C | G | C | G | T | T | A | A | T | C | A | G | C | A |
| 142 | Qy | A | Arg | Asn | Arg | Ser | Ser | Ser | G | L | Y | Ser | Val | Ala | Asn |
| 423 | Db | C | G | T | A | C | G | C | A | T | C | G | A | T | C |
| 162 | Qy | G | L | u | C | L | Y | Thr | Leu | G | L | Y | Thr | Met | Asp |
| 483 | Db | C | A | A | G | G | G | T | T | A | A | C | C | C | T |
| 182 | Qy | Ser | Gly | Ser | Ala | Ser | Ile | Thr | Val | Ser | 190 | | | | |
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RESULT 3

US-08-121-436A-1
Sequence 1, Application US/08121436A
Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko
APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Ritva
APPLICANT: Palcheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Pagarstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: For Their Production
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimballa, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 base pairs

APPLICANT: AOYAGI, KAORU
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 822
TYPE: DNA
ORGANISM: TRICHODERMA VIRIDE MC300-1
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (14)..(112)
FEATURE:
NAME/KEY: CDS
LOCATION: (14)..(112)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (113)..(809)
FEATURE:
NAME/KEY: CDS
LOCATION: (113)..(285)
FEATURE:
NAME/KEY: intron
LOCATION: (286)..(412)
FEATURE:
NAME/KEY: CDS
LOCATION: (413)..(809)
US-09-254-733-8
Alignment Scores:
Pred. No.: 7,95e-95 Length: 822
Score: 919.00 Matches: 176
Percent Similarity: 77.68% Conservative: 5
Best Local Similarity: 75.54% Mismatches: 9
Query Match: 87.86% Indels: 43
DB: 3 Gaps: 1

US-09-990-874b-55 (1-190) x US-09-254-733-8 (1-822)

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QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 173 GGCACCGCGCGGTGACGTACACCAATGCCCCCGCGCGCGTCTCCGTCACCTGGTCC 232
QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLys----- 56
DB 233 AACTCGGCACTTGTTCGGCGCAAGGATGGCAGCCCGCCACCAAGTAAGAC 292
QY 56 ----- 56
DB 293 TATATACACCCACCTCTGACCAACCCCTATCCACGACAGATAATAAACCAAG 352
QY 57 -----AsnLys 58
DB 353 GCGTGAATATCATGGAGAGAGAGTGTGTGATCTAACGGTTTTTGTCTGAACAACAG 412
QY 59 -ValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrG1 78
DB 413 GGTCACTCACTTCTCGGCGCACCTACACCCCAACGCGCAAGTACTCTCTCGTGTACGG 472
QY 78 YTrpSerArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnPr 98
DB 473 CTGGTCCGCGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCCTACAACCC 532

QY 98 oSerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCy 118
DB 533 GTCCACCGCGCGCCCAAGCTGGCGAGGTGACGTCGCGACGCGACGGTCTACGACATCTA 592
QY 118 sArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTr 138
DB 593 CGCACGCGACGCGCTCAACACCGCGCTCCATCGAGGGCACCTCCACCTTTTACCACTACTG 652
QY 138 pSerValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAl 158
DB 653 GTCCGTCCGCGCCACCCACCGCTCCAGCGGTCCGTCAACGCGGACCACTTCCACGC 712
QY 158 atrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluG1 178
DB 713 GTGGGCTTCGCAACGCGCTGACGCTGGGCACCATGGATTACCAAGATTGTTCGCGTGAGGG 772
QY 178 YTrpPheSerSerGlySerAlaSerIleThrValSer 190
DB 773 CTACTTTAGCTCTGGCTCTGCTTCATCACCCTGACG 809

RESULT 5

US-08-768-373-1
Sequence 1, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NTYL, ARJA
APPLICANT: VEHMAANPER, JARI
APPLICANT: LANTTO, RAJJA
APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIRKKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNES, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:

ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "XLNA"
FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "XLNA"
US-08-768-373-1

Alignment Scores:
Pred. No.: 3,1e-68 Length: 1281
Score: 687.00 Matches: 126
Percent Similarity: 72.86% Conservative: 27
Best Local Similarity: 60.00% Mismatches: 36
Query Match: 65.68% Indels: 22
DB: 3 Gaps: 2

US-09-990-874B-55 (1-190) x US-08-768-373-1 (1-1281)

QY 1 GlnThrIle---GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
Db 273 CAGACGCTCACCAGCAGTGCACCGGCACCCACCAATGGCTACTACTACAGCTTCTGGACC 332

QY 20 AspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValaenTtp 39
Db 333 GATGGCCAAAGGCAACATTCGTTCAACCTCGAGAGCGGTGGCCAGTACAGCGTGACATGG 392

QY 40 SerAsnSerGlyAsnPheValGlyGlyLys----- 49
Db 393 TCTGGTAACGGCACTGGGTGTCGGGCAA-AGGTATGTCCTCTTAATGTTTCCAGCGCTA 451

QY 50 -----GlyTtpGlnProGlyThrLysAsnLysVal 59
Db 452 TCGAATGAACCTAAATGCTAACTGTTTAAACAGGCTGGAAACCCCGGTACCGATACCGGTGC 511

QY 60 IleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTtp 79
Db 512 ATCACTACACAGCCGCACTACAGACCAACGGCACTCTCTTACCTCGCGCTACGGCTGG 571

QY 80 SerArgAsnProLeuIleGluTyrTrilleValGluAsnPheGlyThrTyrAsnProSer 99
Db 572 ACCCGCAACCCGCTGATCGAGTACTAGTGTCTGAGAGCTTCGGCACTTACGACCGCTGC 631

QY 100 ThrGlyAlaThrIleHisGlyGluValThrSerAspGlySerValTyrAspIleCysArg 119
Db 632 ACGGGCGCCACCGCGATGGCGAGCTGACCCAGCGCGGCGCACCTACACATCTACCGC 691

QY 120 ThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSer 139
Db 692 ACGCAGCGCTCAACCGCCCTCCATCGAGGGGCAACCAAGACCTTCACCAATCTGGTCT 751

QY 140 ValArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTtp 159
Db 752 GTCGCGCACTCCAGCGCACCGCGGTACTGTTCATGCGCAACCACTTCATGTGG 811

QY 160 AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 812 AGCGAGGCTGGTCTCGAGCTGGGTTCCTCATGATTATCAGATTCTGGCTACTGAGGGTTAC 871

QY 180 PheSerSerGlySerIleThrVal 189
Db 872 TACTCGTCTGGCTCGGCGACTGTCATGTT 901

RESULT 6
US-09-849-242A-1
Sequence 1, Application US/09849242A
Patent No. 6635464
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
HAKOLA, SATU

MONTILO, ARJA
VEHMAANPERO, JARI
LANTTO, RAIJA
LAHTINEN, TARJA
FAGERSTRM, RICHARD
SUONINEN, PIIRKO
TITLE OF INVENTION: NOVEL XILANASES, GENES ENCODING THEM,
AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "XLNA"
FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "XLNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-242A-1

Alignment Scores:
Pred. No.: 3,1e-68 Length: 1281
Score: 687.00 Matches: 126
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Query Match: 65.68% Indels: 22
DB: 3 Gaps: 2

US-09-990-874B-55 (1-190) x US-09-849-242A-1 (1-1281)

QY 1 GlnThrIle---GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn 19
Db 273 CAGACGCTCACCAGCAGTGCACCGGCACCCACCAATGGCTACTACTACAGCTTCTGGACC 332

QY 20 AspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAenTtp 39
Db 333 GATGGCCAAAGGCAACATTCGTTCAACCTCGAGAGCGGTGGCCGTACAGCGTGACATGG 392
QY 40 SerAenSerGlyAenPheValGlyGlyLys----- 49
Db 393 TCTGGTAAACGGCAACTGGGTGGCGCAA- AGGTATGTCTCTTTAATGTTTCCAGCGCTA 451
QY 50 -----GlyTtpGlnProGlyThrLysAenLysVal 59
Db 452 TGGAAATGAACATAATGCTAACTGTTAAACAGCGGTGAACCCCGGTACCGATACCGGTGC 511
QY 60 IleAenPheSerGlySerThrAenProAenGlyAenSerThrLeuAlaValThrGlyTtp 79
Db 512 ATCAATACACAGCCCACTACAGACCAACGGCACTCTTACTCTCCGCTGTACGGCTGG 571
QY 80 SerAenProLeuIleGlyTyrIleValGluAenPheGlyThrTyrAenProSer 99
Db 572 ACCCGCAACCCGCTGATCGAGTACTAGTGTGCGAGAGCTTGGCACTTACGACCCGTCG 631
QY 100 ThrGlyAlaThrLysHisGlyGluValThrSerAenGlySerValThrAspIleCysArg 119
Db 632 ACGGGCGCCACCGCATGGCGAGCGTGACCCAGCGCGGCACCTTACCAATCTTACCGC 691
QY 120 ThrGlnArgValAenAlaProSerIleGlyThrAlaThrPheTyrGlnTyrTtpSer 139
Db 692 ACGAGCGGTCAACCGCCCTCCATCGAGGCGCAACAGACCTTACCACTACTGCTT 751
QY 140 ValArgAenAenArgSerSerGlySerValAenThrAlaAenHisPheAenAlaTtp 159
Db 752 GTGGCGACCTCCAGCGCACCGCGGTACTGTTACCATGGCCCAACCACTTCAATGCTTG 811
QY 160 AlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 812 AGCAGCGCTGCTGCGAGCTGGGTGCCATGATTATCAGATTGTGGCTACTGAGGGTTAC 871
QY 180 PheSerSerGlySerAlaSerIleThrVal 189
Db 872 TACTCGTCTGGCTCGCGGCACTGTCAATGTT 901

RESULT 7

US-08-886-765-1
; Sequence 1, Application US/08886765
; Patent No. 5817500
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullertz, Anette
; APPLICANT: Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5817500 No. 5817500disk of No. 5817500th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Thermomyces lanuginosus
; STRAIN: DSM 4109
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..705
US-08-886-765-1

Alignment Scores:
Pred. No.: 1,828-63 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 2 Gaps: 1

US-09-990-874B-55 (1-190) x US-08-886-765-1 (1-983)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAenGlyTyrPheTyrSerTyrTtpAenAsp 20
Db 124 CAGACAACCCCACTCGGAGGCGCTGGCACGATGGTTATTACTTCTCTGGTGGAGTGAC 193
QY 21 GlyHisGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAenTtpSer 40
Db 184 GTGGAGCGCGCCAGCGTACCAACCTGGAAGCGGCACCTACCGAGATCAGCTGGGA 243
QY 41 AenSerGlyAenPheValGlyLysGlyTtpGlnProGlyThrLysAenLysValIle 60
Db 244 GATGGCGGTAACTCGTGGTGGAAAGGCGTGAACCCCGCGCTGAACCAAGAGCCATC 303
QY 61 AenPheSerGlySerTyrAenProAenGlyAenSerTyrLeuAlaValTyrGlyTtpSer 80
Db 304 CACTTGTAGGGTGTTTACCAGCAACGGCAACAGCTACTTTCGGCTCTACGGTTGGACC 363
QY 81 ArgAenProLeuIleGlyTyrIleValGluAenPheGlyThrTyrAenProSerThr 100
Db 364 CGCAACCCGCTGCTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGluValThrSerAenGlySerValTyrAspIleCysArgThr 120
Db 424 GGTGCTACCGATCTAGGAACCTGCGAGTCGACGCGTAGCATCTATCGACTCGGCAAGACC 483
QY 121 GlnArgValAenAlaProSerIleGlyThrAlaThrPheTyrGlnTyrTtpSerVal 140
Db 484 ACTCGCGTCAACGCGACCTAGCATCGACGCGCAACCAACCTTCGACCAATCTCGTTCGTC 543
QY 141 ArgArgAenArgSerSerGlySerValAenThrAlaAenHisPheAenAlaTtpAla 160
Db 544 CGCCAGGCAACGGCACCGGTACCGTCCAGACGGGCTGGCCACTTCGACGCGCTGGGCT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
Db 604 CGCGCTGCTTGAATGTCAACGCGTGACCACTACTACCAATCGTTCAGATCGTTCGAGGGGCTAC 663
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
Db 664 TTCAGCAGCGGCTATGCTCGCATCACCGGTGCT 696

RESULT 8

US-09-115-660-1
; Sequence 1, Application US/09115660
; Patent No. 6245546
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp

APPLICANT: Wagner, Peter
APPLICANT: Mullert, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62455460 No. 62455460 of No. 6245546th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/886,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambirie, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324-204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
US-09-115-660-1
Alignment Scores:
Pred. No.: 1.82e-63 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 3 Gaps: 1
US-09-990-874b-55 (1-190) x US-09-115-660-1 (1-983)
QY 1 GlnThrIleGlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 124 CAGCAACCCCACTCGGAGGGCTGGCAGCATGTTATTCTCTGGTGGAGTGAC 183
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 184 GGTGAGCGCAGCCACGTACCAACCTGGAGGGCGGCACCTACGAGATCAGCTGGGA 243
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyTrpGlnProGlyThrIleAsnLysValle 60
DB 244 GATGGCGGTAACTCGTGGTAAAGGCTGGAAACCCCGGCTGAACCAAGAGGCAATC 303
QY 61 AsnPheSerGlySerTyrAsnProGlyGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 304 CACTTTGAGGGTGTATTACAGCCAAACGCAACAGCTACCTTCGCGTCTACCGTGGACC 363
QY 81 ArgAsnProIleGlyTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100

DB 364 CGCAACCGCTGGTGGAGTATTATCATGTCGAGAACTTGGCACTATGATCTTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 424 GGTGCTACCGATCTAGGAACGTGCGAGTGGCGAGTATCATCGACTCGGCAAGACC 483
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 484 ACTCGCGTCAACGCACTAGCATCGACGGCAACCCCAACCTTCGACCAATATCTGGTGGTGC 543
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 544 CGCAGGCAAGCGCACCGCGGTACCGTCCAGAGGGCTGCCACTTCGACCGCTGGGT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 604 CGCGCTGGTGGTGAATGTCAACGGTGACCACTACTACCAAGATCGTTGCAACGAGGGCTAC 663
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 664 TTCAGCAGCGCTATGCTCGCATCACCGTTCCT 696
RESULT 9
US-08-768-373-3
; Sequence 3, Application US/08768373
; Patent No. 6228629
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; APPLICANT: HAKOLA, SATU
; APPLICANT: M NYL, ARJA
; APPLICANT: VEHMAANPER, JARI
; APPLICANT: LANTTO, RAIJA
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: PAGERSTR, M, RICHARD
; APPLICANT: SUOMINEN, RIKKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/768,373
; FILING DATE: 17-DEC-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,746
; FILING DATE: 18-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,839
; FILING DATE: 28-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CIMBALA, MICHELE A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0540003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 204..472
OTHER INFORMATION: /product= "XLNB"
FEATURE:
NAME/KEY: exon
LOCATION: 537..960
OTHER INFORMATION: /product= "XLNB"
US-08-768-373-3

Alignment Scores:
Pred. No.: 2,16e-62 Length: 1174
Score: 635.00 Matches: 120
Percent Similarity: 69.76% Conservative: 23
Best Local Similarity: 58.54% Mismatches: 41
Query Match: 60.71% Indels: 21
DB: 3 Gaps: 2

US-09-990-874B-55 (1-190) x US-08-768-373-3 (1-1174)

QY 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsnAspGlyHisGlyGlyVal 25
DB 336 GGCACGGGCACACACACGGGTGGTATTACTCTCTCGACCGCGCGCGCGCGGTG 395
QY 26 ThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTyrSerAsnSerGlyAsnPhe 45
DB 396 TGGTACACCAATGGTAATGGCGGTTCGTATAGTGTGAACCTGGCAGAACTGTGGAAATTTT 455
QY 46 ValGlyGlyGlyGlyTyr-----GlnProGly-ThrLysAsn----- 57
DB 456 GTCCGCGGAAAGGATGGTAAAGCTACTGTCCACCGGACCTGAAACTTAGTGGCGGAC 515
QY 58 -----LysValIleAsnPheSerGlySe 65
DB 516 CAGATGCTGACCTGTCTCCAGCGGCACCGCGCGGCAACGATCAATACTCCGGCAA 575
QY 65 rTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrSerArgAsnProLeu1 85
DB 576 CTACAACCGTCGGCAACAGCTACTCTCGCATCTACGGCTGACGCGCAACCCCTGCT 635
QY 85 eGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrIlyshi 105
DB 636 TGAGTACTACATCGTCGAGTCGTACGGCACTTACGATCCGTCGCGGCGCCAGAACTT 695
QY 105 sGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAl 125
DB 696 GGGCACAATCCAGTCGAGCGGGGACGTACAGATCGCCAGAGCAGCGGGTACATGC 755
QY 125 aProSerIleGluGlyThrAlaThrPheTyrGlnTyrTyrSerValArgAsnArgAr 145
DB 756 TCCTCAATCGAAGGAACCAAGACGTTTACGCAAGTATTCGAGCGTTCGAGCAGCTCAAAGCG 815
QY 145 qSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTyrAlaArgGlnGlyLeuth 165
DB 816 GGTGGAGGACCGGTACCGGTCGCAACCACTTCAATGCTTGAAGAGTAAAGGGGTGAA 875
QY 165 rLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAl 185
DB 876 TTGGGTAGCCACCATTAACAGATTGTGGCACTGAGGGTTATAGAGTAGTGGGTCCGC 935
QY 185 aSerIleThrVal 189
DB 936 TTCGATTACTGTT 948

RESULT 10

US-09-849-242A-3
; Sequence 3, Application US/09849242A
; Patent No. 6635464

GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
HAKOLA, SATU
MONTYLO, ARJA
VEHMAANPERO, JARI
LANTTO, RAIJA
LAHTINEN, TARJA
FAGERSTRIM, RICHARD
SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/POCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
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SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 204..472
OTHER INFORMATION: /product= "XLNB"
FEATURE:
NAME/KEY: exon
LOCATION: 537..960
OTHER INFORMATION: /product= "XLNB"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-849-242A-3
Alignment Scores:
Pred. No.: 2,16e-62 Length: 1174
Score: 635.00 Matches: 120
Percent Similarity: 69.76% Conservative: 23
Best Local Similarity: 58.54% Mismatches: 41
Query Match: 60.71% Indels: 21
DB: 3 Gaps: 2
US-09-990-874B-55 (1-190) x US-09-849-242A-3 (1-1174)

QY 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTTPAsnAspGlyHisGlyGlyVal 25
Db 336 GGCACGGGCACACACACGGGTGGTATTACTCTCTGGACCGACGGCGCGGCACGGTG 395
QY 26 ThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTTPSerAsnSerGlyValPhe 45
Db 396 TGGTACACCAATGGTAATGGCGGTGATAGTGTGAATGGCAGAACTGTGGAAATTTT 455
QY 46 ValGlyGlyLysGlyTTP-----GlnProGly-ThrLysAsn----- 57
Db 456 GTCCGCGGAAGGGATGGTAAGCTCACTCTCCACCGCGACACTGAAACTTAGTGGCGAGC 515
QY 58 -----LysValIleAsnPheSerGlySe 65
Db 516 CAGATGCTGACCTCTGTCCAGCGCACCGCGCGACCGCAACAGCTCAAAATACTCCGGCAA 575
QY 65 rTyraenProAenGlyAenSerTyrlleuAlaValTyrglyTTPSerArgAsnProLeu11 85
Db 576 CTACAAACCGTCCGGCAACAGGTACTCTGCCATCTACGGCTGGACCGCAACCCCTGTGT 635
QY 85 eGluTyTyrIleValGluAsnPheGlyThrTyraenProSerThrGlyAlaThryshi 105
Db 636 TGAGTACTACATCGTCGAGTCGTACGGCACTTACGATCCGTCTCGGGCGCCAGACTT 695
QY 105 sGlyGluValThrSerAspGlySerValTyraenPheGlyCysArgThrGlnArgValAsnAl 125
Db 696 GGGCATTTCAGTTCGACGGCGGACGTACAAGATCGCAAGAGCACGCGGTACAAATGC 755
QY 125 aProSerIleGluGlyThrAlaThrPheTyrglyTTPSerValArgAsnArgAr 145
Db 756 TCCCTCAATCGAAGGAACCAAGACGTTTACGAGTATTGGAGCGTGGAGACGTCAAAGCG 815
QY 145 qSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTTPAlaArgGlnGlyLeuTh 165
Db 816 GGTGGAGCAGCAGGTGACCGTTCGGAACATTTCATATGCTTGGACAGTAAGGGTTGAA 875
QY 165 rLeuGlyThrMetAspTyrglnIleValAlaValGluGlyTyrPheSerSerGlySerAl 185
Db 876 TTTGGGTAGCCACGATTATCAGATTGTGGCGACTGAGGGTTTAAAGTAGTGGGTTCGC 935
QY 185 aSerIleThrVal 189
Db 936 TTCGATTACTGTT 948

RESULT 11
US-08-290-979A-7
; Sequence 7, Application US/08290979A
; Patent No. 5610046
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, Albert J.H.
; APPLICANT: DE GRAAFF, Leendert H.
; APPLICANT: VAN DEN BROECK, Henriette C.
; APPLICANT: VISSER, Jacob
; TITLE OF INVENTION: Cloning and Expression of Xylanase B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,979A
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KATE H. MURASHIGE

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0045.00
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSN FOERS WSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE: ORGANISM: Aspergillus tubigenensis
STRAIN: DSI6813
FEATURE:
NAME/KEY: CDS
LOCATION: join(902..1180, 1248..1643)
US-08-290-979A-7
Alignment Scores:
Pred. No.: 2,268-61 Length: 2219
Score: 629.50 Matches: 116
Percent Similarity: 71.22% Conservative: 30
Best Local Similarity: 56.59% Mismatches: 37
Query Match: 60.18% Indels: 22
DB: 2 Gaps: 1
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Db 1028 ACCGCGGAGAACACACGGCTTCTACTACTCTCTGGACCGACGGCGGTGTGTGACC 1087
QY 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTTPSerAsnSerGlyValAsnPheVal 46
Db 1088 TACACCAACGGGTGACGGTCTCGTACACCGTGGAGTGTGTGTGTGTGTGTGTGT 1147
QY 47 GlyGlyLysGlyTTPGlnProGlyThr-LysAsnLysVal----- 59
Db 1148 GGTGGAAAGGCTGGAAACCTCGGAAGTGGCAGTAAGTTAACCTTTCCCAAGCTGTCCCT 1207
QY 60 -----IleAsnPheSerGlySe 65
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QY 65 rTyraenProAenGlyAenSerTyrlleuAlaValTyrglyTTPSerArgAsnProLeu11 85
Db 1268 CTTTACCCCTAGCGCAACGGCTACTCTCTCGTCTATGGCTGGACCACTGACCCCTGAT 1327
QY 85 eGluTyTyrIleValGluAsnPheGlyThrTyraenProSerThrGlyAlaThryshi 105
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QY 105 sGlyGluValThrSerAspGlySerValTyraenPheGlyCysArgThrGlnArgValAsnAl 125
Db 1388 GGGCAGCGTCACTCCGATGGATCCGCTTACGATATCTACGGCTTACCGCGTACCGCAACGC 1447
QY 125 aProSerIleGluGlyThrAlaThrPheTyrglyTTPSerValArgAsnArgAr 145
Db 1448 CGCTTCCATCCCAAGGAACCGCTTACCTTACCCAGTACTCGTCTCGGTTCGCCAGAACAGAG 1507
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QY 165 rLeuGlyThrMetAspTyrglnIleValAlaValGluGlyTyrPheSerSerGlySerAl 185
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QY 185 aSerIleThrVal 189

Db 1628 CTCATCACTGTT 1640
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US-08-468-812-1
; Sequence 1, Application US/08468812
; Patent No. 5935836
; GENERAL INFORMATION:
; APPLICANT: Vehmaanper, Jari
; APPLICANT: M ntyl, Arja
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lehtinen, Tarja
; APPLICANT: Kristo, Paula
; TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERNE, KESSLER, GOLSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,812
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Larry B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 303..1334
US-08-468-812-1
Alignment Scores:
Pred. No.: 1.25e-59 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservative: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
DB: 2 Gaps: 3
US-09-990-874B-55 (1-190) x US-08-468-812-1 (1-1375)
Qy 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23

Db 447 CAGAACACGCGGTACGACACCGCTACTCTCTCTGACCGCGCGCGG 506
Qy 24 GlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGly 43
Db 507 ACCGHTCTCATGACCTTCATCTCGGCGCGGACGACCTCTGCGGGACACCGG 566
Qy 44 AsnPheValGlyGlyLeuGlyTrpGlnProGlyThrLysAsnLysValleAsnPheSer 63
Db 567 AACTTCGTGCGCGGCAAGGCTGTGTCACCGGGGACGG---CGGACCGTGACCTACAC 623
Qy 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnPro 83
Db 624 GCCTCTTCAACCCGTCGCGGTAAACGCTACCTTCACGCTCTACGCTTGGACCGAGAACCG 683
Qy 84 LeuileGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
Db 684 CTCGTCGAGTACTACATCGTCGAGAGCTGGGCGACCTACCGGCCC---ACCGGCACCTAC 740
Qy 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
Db 741 AAG---GGCACCGTCAACCCGACCGGCGGGAACGTACGACATCTACGAGACCTGGCGGTAC 797
Qy 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgArgAsn 143
Db 798 AACGCGCGGTCCATCGAGGCGCACCGGACCTTCCAGCAGTTCCTGGAGCGTTCGGCAGCAG 857
Qy 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163
Db 858 AAGCGGACCGGCGGACCATCACCATCGGCAACCATTCGACGCTTGGGCGCGCGCGG 917
Qy 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
Db 918 ATGAACCTGGGCGACGACGACTACCGATCATGGGCGCGGAGGCTTACGAGGCTTACGAGCAG 977
Qy 184 SerAlaSerIleThrValSer 190
Db 978 AGCTCCACCGTCTCCATCAGC 998
RESULT 13
US-08-590-563-1
; Sequence 1, Application US/08590563
; Patent No. 6300114
; GENERAL INFORMATION:
; APPLICANT: M ntyl, Arja
; APPLICANT: Vehmaanper, Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lehtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERNE, KESSLER, GOLSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,563
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,812
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536


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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 1050.0340003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1375 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 303..1334
/
US-08-590-563-1
Alignment Scores:
Pred. No.: 1,25e-59 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservatives: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
DB: 3

US-09-990-874B-55 (1-190) x US-08-590-563-1 (1-1375)
Qy 4 GlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23
Db 447 CAGAACACGCGGTGACGACGCGTACTTCTGACGCGCGCGCGCGCGCGG 506

Qy 24 GlyValThrMetLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGly 43
Db 507 ACCGTCCTCATGCCCTCCACTCGGCGCGCGAGTACGACACCTCGTGGCGGACACCGCG 566

Qy 44 AsnPheValGlyGlyValGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSer 63
Db 567 AACTTCGTCCGCGGCAAGCGGTGGTCCACCGGGGGACGG---CGGACCGGTGACCTACAC 623

Qy 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnPro 83
Db 624 GCCTCCTCAACCGCGGTGCGGTACCGCTACCTACCTACGCTTACGGCTGGACCGACCGCG 683

Qy 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
Db 684 CTCGTCGAGTACTACATCGTCGAGAGCTGGGCGACCTACCGGCC---ACCGCGACCTAC 740

Qy 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
Db 741 AAG---GGCACCGTCCACCGCGGGGAAAGTACGACATCTACGAGACCTGGCGGTAC 797

Qy 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsn 143
Db 798 AACGGCGCGTCCATCAGGGGACCCCGGACCTTCCAGCAGTCTTGGAGCGCTCGGCGACGAG 857

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Qy 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
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Qy 184 SerAlaSerIleThrValSer 190
Db 978 AGTCCACCGTCTCCATCAGC 998

RESULT 14
US-09-770-621-1
/ Sequence 1, Application US/09770621
/ Patent No. 6506593
/ GENERAL INFORMATION:
/ APPLICANT: M ntyl , Arja
/ APPLICANT: Vehmaanper , Jari
/ APPLICANT: Pagarstr m, Richard
/ APPLICANT: Lantto, Raija
/ APPLICANT: Palohelmo, Marja
/ APPLICANT: Suominen, Pirkko
/ APPLICANT: Lahtinen, Tarja
/ TITLE OF INVENTION: Production and Secretion of Proteins of
/ NUMBER OF SEQUENCES: 39
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
/ STREET: 1100 New York Ave., N.W. Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/09/770,621
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/590,563
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 1050.0340003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1375 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: No. 6506593 Relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 303..1334
/
US-09-770-621-1
Alignment Scores:
Pred. No.: 1,25e-59 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservatives: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
DB: 3
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US-09-990-874B-55 (1-190) x US-09-770-621-1 (1-1375)

Qy 4 GlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23
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Db 447 CAGAACACGACGGGTACGACAACGGCTACTTCTACTCGTTCTGGACCGACGCCGCGG 506

Qy 24 GlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGly 43
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Db 507 ACCGTCTCCATGACCCTCCACTCGGCGCGAGTACAGCACCTCGTGGCGGAACACCGG 566

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Db 567 AACTTCGTGCGCGCAAGGGCTGTGCACCGGGGACCG---CGGACCGTGACCTTACAC 623

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|||
Db 624 GCCTCCTTCAACCGCTCGGGTAACGGCTACCTCACGCTCTACGGCTGGACCAAGAACCG 683

Qy 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
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Db 684 CTCGTGAGTAGTACTACATCGTCGAGAGCTGGGGCACTACCGGCC---ACCGGCACTTAC 740

Qy 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
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Db 741 AAG---GGCACCGTACACCCACCGACGGGGAAAGTACAGCATCTACAGAGACCTGGCGGTAC 797

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Qy 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
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Db 918 ATGAACCTGGGCAGCCAGCATACCATGATGCGGCAACCGAGGGCTACAGAGCAGCGGT 977

Qy 184 SerAlaSerIleThrValSer 190
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Db 978 AGTCCACCGTCTCCATCAGC 998

RESULT 15
US-09-235-832-1
; Sequence 1, Application US/09235832
; Patent No. 6667170
; GENERAL INFORMATION:
; APPLICANT: M ntyl , Arja
; APPLICANT: Vehmaanper , Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,832
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 02:30:46 ; Search time 808 Seconds

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Title: US-09-990-874B-55

Perfect score: 1046

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Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 974 | 93.1 | 596 | US-10-307-441-39 | Sequence 39, Appl |
| 2 | 679.5 | 65.0 | 818 | US-10-425-115-37173 | Sequence 37173, A |
| 3 | 664.5 | 63.5 | 705 | US-10-213-990-68 | Sequence 68, Appl |
| 4 | 659.5 | 63.0 | 850 | US-10-425-115-177283 | Sequence 177283, |
| 5 | 648 | 62.0 | 739 | US-10-213-990-67 | Sequence 67, Appl |
| 6 | 643.5 | 61.5 | 588 | US-10-237-386-9 | Sequence 9, Appl |
| 7 | 643.5 | 61.5 | 678 | US-09-803-454-3 | Sequence 3, Appl |

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|----|-------|------|-------|----|---------------------|-------------------|
| 8 | 643.5 | 61.5 | 983 | 3 | US-09-467-368-1 | Sequence 1, Appl |
| 9 | 638 | 61.0 | 942 | 5 | US-10-213-990-71 | Sequence 71, Appl |
| 10 | 627 | 59.9 | 1002 | 5 | US-10-213-990-70 | Sequence 70, Appl |
| 11 | 625.5 | 59.8 | 666 | 5 | US-10-213-990-65 | Sequence 65, Appl |
| 12 | 625.5 | 59.8 | 749 | 8 | US-10-425-115-82922 | Sequence 82922, A |
| 13 | 611.5 | 58.5 | 1375 | 3 | US-09-770-621-1 | Sequence 1, Appl |
| 14 | 611.5 | 58.5 | 1375 | 6 | US-10-286-993-1 | Sequence 1, Appl |
| 15 | 605.5 | 57.9 | 2898 | 5 | US-10-299-393-1 | Sequence 1, Appl |
| 16 | 605.5 | 57.9 | 2898 | 10 | US-11-154-793-1 | Sequence 64, Appl |
| 17 | 605 | 57.8 | 712 | 5 | US-10-213-990-64 | Sequence 8, Appl |
| 18 | 584.5 | 55.9 | 2225 | 3 | US-09-790-070A-8 | Sequence 3, Appl |
| 19 | 554.5 | 53.0 | 591 | 10 | US-11-018-645-3 | Sequence 17, Appl |
| 20 | 554.5 | 53.0 | 594 | 10 | US-11-018-645-17 | Sequence 10, Appl |
| 21 | 554.5 | 53.0 | 628 | 10 | US-11-018-645-10 | Sequence 21, Appl |
| 22 | 554.5 | 53.0 | 978 | 10 | US-11-018-645-21 | Sequence 5, Appl |
| 23 | 549 | 52.5 | 972 | 10 | US-11-018-645-5 | Sequence 5, Appl |
| 24 | 549 | 52.5 | 972 | 10 | US-11-018-645-19 | Sequence 19, Appl |
| 25 | 549 | 52.5 | 1009 | 10 | US-11-018-645-11 | Sequence 11, Appl |
| 26 | 502 | 48.0 | 555 | 10 | US-11-018-645-1 | Sequence 1, Appl |
| 27 | 502 | 48.0 | 561 | 10 | US-11-018-645-13 | Sequence 13, Appl |
| 28 | 502 | 48.0 | 598 | 10 | US-11-018-645-9 | Sequence 9, Appl |
| 29 | 502 | 48.0 | 8537 | 10 | US-11-018-645-34 | Sequence 34, Appl |
| 30 | 502 | 48.0 | 8546 | 10 | US-11-018-645-33 | Sequence 33, Appl |
| 31 | 502 | 48.0 | 12763 | 10 | US-11-018-645-35 | Sequence 35, Appl |
| 32 | 501.5 | 47.9 | 642 | 8 | US-10-626-583-4 | Sequence 4, Appl |
| 33 | 501.5 | 47.9 | 642 | 9 | US-10-626-724-4 | Sequence 4, Appl |
| 34 | 500 | 47.8 | 642 | 9 | US-10-626-583-10 | Sequence 10, Appl |
| 35 | 500 | 47.8 | 642 | 8 | US-10-626-583-12 | Sequence 12, Appl |
| 36 | 500 | 47.8 | 642 | 9 | US-10-626-724-10 | Sequence 10, Appl |
| 37 | 500 | 47.8 | 642 | 9 | US-10-626-724-12 | Sequence 12, Appl |
| 38 | 499 | 47.7 | 642 | 8 | US-10-626-583-8 | Sequence 8, Appl |
| 39 | 499 | 47.7 | 642 | 9 | US-10-626-724-8 | Sequence 8, Appl |
| 40 | 497 | 47.5 | 642 | 8 | US-10-626-583-6 | Sequence 6, Appl |
| 41 | 497 | 47.5 | 642 | 9 | US-10-626-724-6 | Sequence 6, Appl |
| 42 | 497 | 47.5 | 645 | 6 | US-10-237-386-10 | Sequence 10, Appl |
| 43 | 497 | 47.5 | 657 | 6 | US-10-237-386-11 | Sequence 11, Appl |
| 44 | 489 | 46.7 | 663 | 3 | US-09-909-207-1 | Sequence 1, Appl |
| 45 | 489 | 46.7 | 663 | 3 | US-09-909-207-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1

US-10-307-441-39
; Sequence 39, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Trx
US-10-307-441-39

Alignment Scores: 8.65e-112 Length: 596
Pred. No.: 974.00 Matches: 179
Score: 96.32% Conservativeness: 4
Percent Similarity: 94.21% Mismatches: 7
Best Local Similarity: 94.21%

```
Query Match: 93.12% Indels: 0
DB: 6 Gaps: 0
US-09-990-874B-55 (1-190) x US-10-307-441-39 (1-596)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 23 CAACAAATACACAGGAAACCGGTTACAAACAGCGTTACTTTTACAGCTATTGGAAACGAT 82
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 83 GGCATGGTGGTGTACCTATACAAACCGGCGCGGAGGCCAATTTAGCGTCATATTGGTCT 142
QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 143 AACTCCGGAACCTTCGTAGTGGAAAGGTGGCAACCCCGGAGCAAAAATAAGGTGATC 202
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 203 AACTTCTCTGGATCTTATAATCCGAATGGGAATTCATCTTAAGCGTCTATGGCTGTCT 262
QY 81 ArgAsnProLeuIleGluTyrTrileValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 263 AGAAACCCACTGATTGAATATTACATGTGCAAAATTTGGTACCTTACAAATCCGATACC 322
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 323 GCGCCACCAAAATTAGCGAGTCACTAGTAGGATCGGTATATGATATCTACCGTACC 382
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 383 CAACGCGTTAATCAGCAGCATCGATCANTGGAAACCGCCACCTTTTATCAGTACTGGAGTGT 442
QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 443 AGACGTAATCATCGGAGCTCCGGTTCGGTTAATACCTGCGGAATCATTATGATCGATGGCA 502
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
DB 503 CAGCAAGGTTAAACCTAGTACAATGGATTATCAAAATCGTAGCGTGGAGGCTACTTTC 562
QY 181 SerSerGlySerAlaSerIleThrValSer 190
DB 563 TCGAGTGGTTCGGCTAGTATTACAGTGAGC 592

RESULT 2
US-10-425-115-37173
; Sequence 37173, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 37173
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133906C.1
US-10-425-115-37173

Alignment Scores: 1.05e-74 Length: 818
Pred. No.: 679.50 Matches: 121
Percent Similarity: 78.42% Conservative: 28
Best Local Similarity: 63.68% Mismatches: 40
```

```
Query Match: 64.96% Indels: 1
DB: 8 Gaps: 1
US-09-990-874B-55 (1-190) x US-10-425-115-37173 (1-818)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 185 CAGACAGCCCCCAACCGCGAAGGAACACACACAGCGCTGCTTCTACTCTTTGGTGGATGAT 244
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 245 GGTGCTCCAGGTACTTACACCAACGGTGCAGGTGGCAGCTACAGCTCACTGGGGA 304
QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 305 AGCGCGGCGCACTTTTGGTGGTAAGGCTGGAACCCCTGGATCGGCC---CGCACCGTT 361
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 362 ACCTACTCGGGCTCTACACACCCCAACCGCAACTCTTACCTTGCCATCTATGGTGGACA 421
QY 81 ArgAsnProLeuIleGluTyrTrileValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 422 CGTAACCTCTCTGTCGAATACCTATGCTGTGGAACCTTCGGAACCTATGACCGAGTTCC 481
QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 482 CAGGCTAGCAACAAGGCTACCGTGAGTCCGACGGCTCTTCTCAAGATCGCTAGTGG 541
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 542 ACCCGTACTTAACACCCATCCATCATGGAACAAGGACCTTTTCAGCAGTACTGGTCTGT 601
QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 602 CCGCAGACAGCGCTCCAGCGATCCGTGAACATGAAGACTCACTTCGATGCTTGGGCC 661
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPhe 180
DB 662 AGCAAGGCGCATGACTCTTGGTAGCCACTACTACCAAGATTGTCGCTACCGAGGATCTTC 721
QY 181 SerSerGlySerAlaSerIleThrValSer 190
DB 722 TCCACCGGTTCTGCTCTATCATCTACTGTGAAC 751

RESULT 3
US-10-213-990-68
; Sequence 68, Application US/10213990
; Publication NO. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (705)
US-10-213-990-68

Alignment Scores: 6.46e-73 Length: 705
Pred. No.: 664.50 Matches: 118
```

| | | | |
|------------------------|--------|---------------|----|
| Percent Similarity: | 76.17% | Conservative: | 27 |
| Best Local Similarity: | 62.18% | Mismatches: | 41 |
| Query Match: | 63.05% | Indels: | 5 |
| DB: | 8 | Gaps: | 2 |

| | | | |
|--|-----|--|---|
| US-09-990-874B-55 (1-190) x US-10-425-115-177283 (1-850) | | | |
| Qy | 2 | ThrIleGlnProGlyThr----- | -GlyTyrHisAspGlyTyrPheTyrSerTyr 17 |
| | | : | |
| Db | 210 | ACTGCACGTCGCGGTACCC | CAGTCCAGGGCACCCACACGGCTGCTTCTACTCTCTGG 269 |
| Qy | 18 | TrpAsnAspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerVal 37 | |
| | | | |
| Db | 270 | TGGACCGACGGTGGCGCC | AGGCTACCTACCAACGAGGCGCGCGCAAGTACACAGCGTC 329 |
| Qy | 38 | AsnTrpSerAsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsn 57 | |
| | | | |
| Db | 330 | AAC TGG AAG ACC GGT GGT TAA | CAT GGT TGG T GGA AAG GGT TGA AAC CCT TGG TCG GGC C --- 386 |
| Qy | 58 | LysValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyr 77 | |
| | | : | |
| Db | 387 | CGCACCATACCTACTCCG | TACTACAGCCGCCAGGGTAACTCTCTACTCTGCCACTCTAC 446 |
| Qy | 78 | GlyTrpSerArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsn 97 | |
| | | | |
| Db | 447 | GGCTGGACCCGCAACCC | CTTGTTCGAGTACTACGTTGTTGAGAACTTTGGTACTTACCGAC 506 |
| Qy | 98 | ProSerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIle 117 | |
| | | : | |
| Db | 507 | CCGTCTCTCGCGCCAGCGT | CAAGGGCTCCGTCACCGCAGACGGCTCGTCTCTACAAGATT 566 |
| Qy | 118 | CysArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyr 137 | |
| | | : | |
| Db | 567 | GGCGACACTCAGCGTGTCAAC | CAGCCCTCCATCGACGCGCACCCAGACCTTCAACCAAGTAC 626 |
| Qy | 138 | TrpSerValArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsn 157 | |
| | | : | |
| Db | 627 | TGGTCCGTTCGCGCAAGAAC | AGCGAGCTCCCGGCTCCGTCACATGAGAACCCACCTTCGAC 686 |
| Qy | 158 | AlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGlu 177 | |
| | | : | |
| Db | 687 | GCCTGGGCGCCCAAGGCGAT | CGCTCGGTCAAGCAACTACCCAGATCGTCCGCCACCGAG 746 |
| Qy | 178 | GlyTyrPheSerSerGlySerAlaSerIleThrValSer 190 | |
| | | : | |
| Db | 747 | GGTTACTTCTCTCCG | CAGCTCGCTCGATCAACCGTTACT 785 |

```

RESULT 5
US-10-213-990-67
; Sequence 67, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTR
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 739
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-67

Alignment Scores:
Pred. No.: 8.04e-71 Length: 739
Score: 648.00 Matches: 118
Percent Similarity: 72.50% Conservative: 27

```

Best Local Similarity: 59.00%
Query Match: 61.95%
DB: 5
MisMatches: 38
Indels: 17
Gaps: 1

US-09-990-874B-55 (1-190) x US-10-213-990-67 (1-739)

QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThr 26
DB 136 ACCGGCTGGAAACAGCGCTACTACTCTCTGAGCTGATGGCGGCGAGCTGACC 195
QY 27 MetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
DB 196 TACACCAATGGCGCGCTGCTGCTACTCGCTCACTGGAGGAACGCTGGCAACTTTGTC 255
QY 47 GlyGlyValGlyTyrGlnProGlyThr-----55
DB 256 GGTGGAAAGCGCTGGAACCCCTGGAAAGCGCTAGTACCGAGCTTTGTCAACGTCGAGATGTG 315
QY 56 -----LysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnG1 70
DB 316 CAGACCTGGCTGGACAGAGTAGAACCATCACTACGGAGGCGAGCTTCAACCCGAGCGG 375
QY 70 YAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGluTyrTrpVal 90
DB 376 CAATGCTACCTGGCTGTCTAGCGCTGGACCAACCCCTTGATTGAGTACTACGTTGT 435
QY 90 lGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGlyValThrse 110
DB 436 TGAGTGGTATGTTGATACATCAACCCCGCAGCGCGGTACCTTCAGGGCGCACTGTCAACAC 495
QY 110 rAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluG1 130
DB 496 CGACGGTGGCACTTACACATCTACACGGCGGTTCGCTACATGCTCCCTCCATCGAGG 555
QY 130 YThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerGlySerVa 150
DB 556 CACCAGACCTTCACCCAGTACTGCTGTGGCACCTCCAGCGTACCGCGGCACTGT 615
QY 150 lAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAs 170
DB 616 CACCATGGCCACCACTTCAACCGCTGGAGCAGACTGGGCATGAACCTGGGAACTCACA 675
QY 170 pTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
DB 676 CTACCAAGATTGTGCCCACTGAGGCTTACCAAGAGCGGGAICTGCTTCCATCACTGTC 733

RESULT 6

US-10-237-386-9
; Sequence 9, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanuginosus

US-10-237-386-9
Alignment Scores:
Pred. No.: 2.62e-70 Length: 678

Pred. No.: 2.15e-70 Length: 588
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 6 Gaps: 1

US-09-990-874B-55 (1-190) x US-10-237-386-9 (1-588)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 4 CAGACAAACCCCAACTCGGAGGCGCTGGCACGATGGTTATTACTTCTTGGTGGAGTGAC 63
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 64 GGTGGAGCGCGCCACGTCACCAACCTGGAAAGCGCGCACCTACGAGATCAGCTGGGA 123
QY 41 AsnSerGlyAsnPheValGlyGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 124 GATGGCGGTAACTCGCTCGTGGAAAGGCGCTGGAACCCCGCGCTGAACGCAAGAGCATC 183
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 184 CACTTTGAGGGTGTTTACCGCAACGCAACAGCTACTTGGCGTCTACGCTTGGACC 243
QY 81 ArgAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 244 CGCAACCCCGCTGGTGGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTCTCC 303
QY 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 304 GGTGCTACCGATCTAGGAACCTGTCGAGTGGCAGCGTAGCATCTATCGACTCGGCAAGACC 363
QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 364 ACTCGCGTCAACGCACTAGCATGCGACGCGCAACCAACCTTCGACCAATACTGTCGTC 423
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 424 CGCCAGGACAGCGCACACGAGCGGTACCGTCCAGACGCGGCTGCCACTTCGACGCTGGCT 483
QY 161 ArgGlnGlyLeuThrIleu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 484 CGCGCTGGTTTGAATGTCAACGTCAGCTACCTACTACGATCGTTGCAACGAGGGGCTAC 543
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 544 TTCAGCAGCGGCTATGCTCGCATCACCGTGTCT 576

RESULT 7

US-09-803-454-3
; Sequence 3, Application US/09803454
; Publication No. US20030022280A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030022280A1ozymes A/S
; APPLICANT: Takagi, Shinobu
; APPLICANT: Terui, Yuri
; TITLE OF INVENTION: High Expression of Industrial Enzymes
; FILE REFERENCE: 6125.200-US
; CURRENT APPLICATION NUMBER: US/09/803,454
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic

US-09-803-454-3
Alignment Scores:
Pred. No.: 2.62e-70 Length: 678

Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 3 Gaps: 1

US-09-990-874B-55 (1-190) x US-09-803-454-3 (1-678)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 94 CAACACCTCCAAATTCGAGGTTGGCATGATGTTATATATATCTTGGTGGTCTGAT 153
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 154 GGTGGTGCTCAAGTACTATATACTAATTTAGAGGTTGGTACCTATGAAATTTCTTGGGT 213
QY 41 AsnSerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 214 GATGGTGGTAATTTAGTGGTAAAGGTTGGAATCCAGGTTTAAATCAAGAGCTATT 273
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 274 CATTTTGAAGGTTTATACCAAAATGTAATCTTATTTAGCTGTTTATGTTGGACT 333
QY 81 ArgAsnProLeuIleGlyTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 334 AGAATCCATTAGTTGAATATTATATTTGTTGAAATTTTGGTACTTATGATCCATCTTCT 393
QY 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspLysCysArgThr 120
DB 394 GGTGCTACTGATTTAGTACTGTTGAATGATGATGTTCTTATTTATAGATTAGTAAACT 453
QY 121 GlnArgValAsnAlaProSerIleGlyGlyThrAlaThrPheTyrGlnTrpSerVal 140
DB 454 ACTAGAGTTAATGCACCATCTATGATGATCTCAAACTTTCATCAATTTGTTCTGT 513
QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 514 AGACAAGATAAAGAACTTCTGTACTGTTCAAACTGGTGTGTCATTTGCTGGGCT 573
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 574 AGAGCTGGTGTGAATGTTAATGGTGATCATATTATATCAAAATTTGTTCAACTGAAGGTTAT 633
QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 634 TTCTCTTCTGGTTATGCTAGAAATTACTGTGCT 666

RESULT 8

US-09-467-368-1
; Sequence 1, Application US/09467368
; Patent No. US20020160080A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; Mullertz, Anette
; Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020160080A10 No. US20020160080A1disk of No. US200201600
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,368

; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Thermomyces lanuginosus
; STRAIN: DSM 4109
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..705
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-467-368-1

Alignment Scores:
Pred. No.: 4,368-70 Length: 983
Score: 643.50 Matches: 117
Percent Similarity: 74.87% Conservative: 26
Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 3 Gaps: 1

US-09-990-874B-55 (1-190) x US-09-467-368-1 (1-983)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
DB 124 CAGACNACCCCACTCGAGGGCTGGCAGATGTTTACTATTCTCTGGTGGAGTGAC 183
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 184 GGTGAGCGCAGGCCACGTCACCAACCTCGAAGCGCGCACCTACGAGATCAGCTGGGA 243
QY 41 AsnSerGlyAsnPheValGlyGlyGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 244 GATGCGGTAACTCTGCTGGTGGAAAGGGCTGGAAACCCCGCGCTGAACGCAAGAGCCATC 303
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
DB 304 CACTTTGAGGGTGTTCACGCCAAACGCGCAACAGCTACCTTGGCTTACGGTTGGACC 363
QY 81 ArgAsnProLeuIleGlyTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 364 CGCAACCGCTGGTGGTATACATCGTCGAGAATTTGGCACCTATGATCTCTCTCC 423
QY 101 GlyAlaThrLysHisGlyGlyValThrSerAspGlySerValTyrAspLysCysArgThr 120
DB 424 GGTGTACCGATCTAGGAACCTGTCCAGTCCGCGTATGATCTATCGACTCGCAAGACC 483
QY 121 GlnArgValAsnAlaProSerIleGlyThrAlaThrPheTyrGlnTrpSerVal 140
DB 484 ACTCGGTCACGCGACCTAGCATCGACGCCCAACCTTCGACCACTACTGTCGGTC 543
QY 141 ArgArgAsnArgSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 544 CGCCAGGACAAGCGCACCGCGGTACCGTCCAGAGCGGCTGCCACTTCGACGCTGGGCT 603
QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 604 CGCGCTGGTGTGAATGTCAACGGTGACCACTACTACAGATCGTTTGAACGAGGGGTAC 663

Db 574 TCCATCCGCCAAACACAGCGATCCAGCGGCACAGCTACCCACCGCAATCCTTCAAGGCC 633
Qy 159 TtpalaaGingLeuThrLeuGlyThrMetAspTyrGlnIleValalaValGluGly 178
Db 634 TGGGCTAGCTGGGGATGAACTGGGTACCCATACTATCAGATTGTTCCACTGAGGGA 693
Qy 179 TyrPheSerSerGlySerAlaSerIleThrValSer 190
Db 694 TATGAGACGACGGGTACCTCGACCATCATCTGCTCG 729
RESULT 11
US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(666)
US-10-213-990-65
Alignment Scores:
Pred. No.: 4,59e-68 Length: 666
Score: 625.50 Matches: 111
Percent Similarity: 77.11% Conservative: 31
Best Local Similarity: 60.33% Mismatches: 41
Query Match: 59.80% Indels: 1
Gaps: 5
US-09-990-874B-55 (1-190) x US-10-213-990-65 (1-666)
Qy 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
Db 115 ACTGGCACGAATAACGGCTACTACTCTCTTGGACCGACGGCGCGCCAGGTGACC 174
Qy 27 MetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
Db 175 TACACCAACGGCAATGGCGCGCATGATACAGTGCATCGGAACAACCTGGCGCACTTTGTT 234
Qy 47 GlyGlyLeuGlyTyrGlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyr 66
Db 235 GCTGGAGAGGCTTGGAAACCGCGCCACGAG--AAAGCGGTACCTACAGCGGCTCTCG 291
Qy 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTyrPheSerArgAsnProLeuIleGlu 86
Db 292 CAGACCAGCGAAACCGGTACCTCTCGGTGACGGCTGGACGACCACTGCGGTGCGAA 351
Qy 87 TyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGly 106
Db 352 TTCTATACGTGGAGATTACGGCTCTATGACCTCTCCACGGAGGCCACCACTCCGCG 411
Qy 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
Db 412 ACCGTGAGAGCGACGGGCGCCAGTACACCTCTACAGACGACGGCGGACGATGCGCG 471
Qy 127 SerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSer 146
Db 472 TCCATCCAGGCGACCGCTACTTTTACAGGACTCTGTGCTCGGTTCGGACTTCGACCGCGAG 531

Qy 147 SerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeu 166
Db 532 AGTGGAACTGTGACGACGAGAACCACTTGTATCGTGGAGAAATGCGGGTCTGCATTTG 591
Qy 167 GlyThrMetAspTyrGlnIleValalaValGluGlyTyrPheSerSerGlySerAlaSer 186
Db 592 GGGAACTTTGACTATATGATTTGTTCCGACGAGGGGTACACAGACGAGCGGCTCTGCTACT 651
Qy 187 IleThrValSer 190
Db 652 ATCACTGTTTCT 663
RESULT 12
US-10-425-115-82922
; Sequence 82922, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 82922
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(749)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_175642C.1
US-10-425-115-82922
Alignment Scores:
Pred. No.: 5,39e-68 Length: 749
Score: 625.50 Matches: 113
Percent Similarity: 73.68% Conservative: 27
Best Local Similarity: 59.47% Mismatches: 49
Query Match: 59.80% Indels: 1
Gaps: 8
US-09-990-874B-55 (1-190) x US-10-425-115-82922 (1-749)
Qy 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAsp 20
Db 170 CAGAACACCCCAACCGCGAGGGTACCCACACCGCTGCTTCTGGTCTTTGGTGGTCTGAT 229
Qy 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
Db 230 GCGCGTGGCGCGCTACCTACACCAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 289
Qy 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
Db 290 AGCGGTGGCAACCTCGTGGTGGAAAGGATGGAAACCCAGGAACCTGCC---CGTACCATC 346
Qy 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSer 80
Db 347 ACCTACTCTGTTACTTACAACTACAAACGGCACTCTACTTGGCTCTTACGGCTGGACC 406
Qy 81 ArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThr 100
Db 407 CGCAACCCCTTTCGAGTACTACGTGTGAGAACTTCGCGACCTTACGACCCCTCTCC 466
Qy 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
Db 467 CAGTCCCAGAACACAGGGTACCGTCACTCTGATGGATCTTCTTCAAGATCGCTCAGTCG 526

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QY 121 GlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyxGlnTyTrpSerVal 140
Db 527 ACCCGTACCAACAGCCCTCCATCGATGCGACGACGACCTTTTCAGCAGTATTGGTCTGTT 586
QY 141 ArgArgAsnArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
Db 587 CGTCAGAACAGCGCTCTTCGCGCTCCGTCATATGAAGACTCACCTTTGACGCCCTGGGCC 646
QY 161 ArgGlnGlyLeuThrLeuGlyThrMetAspTyTrpGlnIleValAlaValGluGlyTyTrpPhe 180
Db 647 ACCAAGGCGATGAACCTTGGCCAGCACTACTACCGATTTGGTCCACCGANGTTACTTC 706

QY 181 SerSerGlySerAlaSerIleThrValSer 190
Db 707 TCCACTGTTAACGGCCAGATCACCGTCAAC 736

RESULT 13
US-09-770-621-1
; Sequence 1, Application US/09770621
; Patent No. US20010024815A1
; GENERAL INFORMATION:
; APPLICANT: M ntyla, Arja
; APPLICANT: Vehmaanper, Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,621
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/590,563
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: No. US20010024815A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 303..1334
US-09-770-621-1
Alignment Scores:
Pred. No.: 7,05e-66 Length: 1375
Score: 611.50 Matches: 108
Percent Similarity: 75.94% Conservative: 34
Best Local Similarity: 57.75% Mismatches: 42
Query Match: 58.46% Indels: 3
DB: 3 Gaps: 3

US-09-990-874B-55 (1-190) x US-09-770-621-1 (1-1375)
QY 4 GlnProGlyThrGlyTyTrpHisAspGlyTyTrpPheTyTrpAsnAspGlyHisGly 23
Db 447 CAGAACCAACGCGGTACGACACACGGCTACTTCTACTCGTTCTGGACCGCGCCGGG 506
QY 24 GlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsnSerGly 43
Db 507 ACCGTCTCCATGACCCCTCCACTCGCGGCGGACGCTACAGCACCTCGTGGCGGAACACCGGG 566
QY 44 AsnPheValGlyGlyTyTrpGlnProGlyThrLysAsnLysValIleAsnPheSer 63
Db 567 AACTTCGTGCGCGCAAGGGCTGTGCCACCGGGGACCG---CGACCGTGACCTACACAC 623
QY 64 GlySerTyTrpAsnProAsnGlyAsnSerTyTrpLeuAlaValTyTrpSerArgAsnPro 83
Db 624 GCCTCTTCAACCCGTCGGGTAAACGGCTACCTACCGCTCTACGGCTGACCGAGAACCCG 683
QY 84 LeuIleGlyTyTrpIleValGluAsnPheGlyThrTyTrpAsnProSerThrGlyAlaThr 103
Db 684 CTCGTGAGTACTACATCGTCGAGAGCTGGGGCACCTACCGGCC---ACCGGCACCTTAC 740
QY 104 LysHisGlyGluValThrSerAspGlySerValTyTrpAspIleCysArgThrGlnArgVal 123
Db 741 AAG---GGCACCGTCACCCAGCGGGGAAACGTACGACATCTACGAGACCTGGCGGTAC 797
QY 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyTrpGlnTyTrpSerValArgAsn 143
Db 798 AACGCGCGTCCATCGAGGGGACCCGAGCCTTCCAGCAGTTCCTGGAGGCTCGGCGACGAG 857
QY 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163
Db 858 AAGCGGACGACGCGCACCATCATCGGCAACCACTTCGACGCGCTGGCGCCCGCCCGCCG 917
QY 164 LeuThrLeuGlyThrMetAspTyTrpGlnIleValAlaValGluGlyTyTrpPheSerSerGly 183
Db 918 ATGAACCTGGGCGACGACGACTACGATCATGCGACCGAGGGGCTACGAGACGCGGT 977
QY 184 SerAlaSerIleThrValSer 190
Db 978 AGCTCCACCGTCTCCATCAGC 998

RESULT 14
US-10-286-993-1
; Sequence 1, Application US/10286993
; Publication No. US20030148453A1
; GENERAL INFORMATION:
; APPLICANT: M ntyla, Arja
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lantto, Raija
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Vehmaanpera, Jari
; TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
; FILE REFERENCE: 1716.0340004
; CURRENT APPLICATION NUMBER: US/10/286,993
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/120,804
; PRIOR FILING DATE: 1998-07-23
```

APPLICANT: Haigh, Nigel Paterson
TITLE OF INVENTION: PENICILLIUM FUNICULOSUM STRAIN USEFUL
FILE REFERENCE: A32917-PCT-USA-I (072667.0183)
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 09/462,246
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: EPO 9801161.5
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1

TYPE: DNA
ORGANISM: Penicillium funiculosum
FEATURE:
NAME/KEY: CDS
LOCATION: (1317) ... (1589)
FEATURE:
NAME/KEY: Intron
LOCATION: (1590) ... (1642)
FEATURE:
NAME/KEY: CDS
LOCATION: (1644) ... (2042)
FEATURE:
NAME/KEY: RBS
LOCATION: (570) ... (576)
FEATURE:
NAME/KEY: RBS
LOCATION: (724) ... (730)
US-10-299-393-1

Alignment Scores:
Pred. No.: 1,118-64 Length: 2898
Score: 605.50 Matches: 109
Percent Similarity: 69.65% Conservative: 31
Best Local Similarity: 54.23% Mismatches: 44
Query Match: 57.89% Indels: 17
DB: 5 Gaps: 1

US-09-990-874B-55 (1-190) x US-10-286-993-1 (1-1375)

QY 4 GlnProGlyThrGlyHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGly 23
DB 447 CAGAACGACGCGGTACGACGCGGTACTTCTCTGTTCTGGACCGCGCGCGG 506
QY 24 GlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGly 43
DB 507 ACCGTCCTCATGACCTCCACTCGGCGCGGAGTACGACGACCTCTGGCGGAACACCGG 566
QY 44 AsnPheValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValLleAsnPheSer 63
DB 567 AACTTGTCTGCGCGGCAAGGCTGTCTCCACCGCGGAGCGG---CGGACCGTGTACCTACAC 623
QY 64 GlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnPro 83
DB 624 GCCTCTCTCAACCGGTGCGGTACCGCTACCTCAGCGCTGTACGCGTGGACCGGACCGG 683
QY 84 LeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThr 103
DB 684 CTCGTCGAGTACTACATCTCGAGACTCGGACCTACCGGCC---ACCGCACCTAC 740
QY 104 LysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgVal 123
DB 741 AAG---GGCACGCTCACACCGGCGGGAACGTACGACATCTACGAGACCTGGCGGTAC 797
QY 124 AsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsn 143
DB 798 AACGCGCGCTCCATCGAGGCGACCGGACCTTCCAGCAGTTCTGGAGCGGTGCGGACGAG 857
QY 144 ArgArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGly 163
DB 858 AAGCGGACCGGCGGACCATCATCCATCGGCGACCATCTTCGACGCTTGGCGCGCGCGG 917
QY 164 LeuThrLeuGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGly 183
DB 918 ATGAACCTGGGCGAGCCACGACTACCATCATGCGGCGGAGGCTTACGAGACGCGGT 977
QY 184 SerAlaSerIleThrValSer 190
DB 978 AGCTCCACCGTCTCCATCAGC 998

RESULT 15

US-10-299-393-1
Sequence 1, Application US/10299393
Publication No. US20030108642A1
GENERAL INFORMATION:
APPLICANT: Sabatier, Alain
APPLICANT: Fish, Neville Marshall

APPLICANT: Haigh, Nigel Paterson
TITLE OF INVENTION: PENICILLIUM FUNICULOSUM STRAIN USEFUL
FILE REFERENCE: A32917-PCT-USA-I (072667.0183)
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 09/462,246
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: EPO 9801161.5
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
TYPE: DNA
ORGANISM: Penicillium funiculosum
FEATURE:
NAME/KEY: CDS
LOCATION: (1317) ... (1589)
FEATURE:
NAME/KEY: Intron
LOCATION: (1590) ... (1642)
FEATURE:
NAME/KEY: CDS
LOCATION: (1644) ... (2042)
FEATURE:
NAME/KEY: RBS
LOCATION: (570) ... (576)
FEATURE:
NAME/KEY: RBS
LOCATION: (724) ... (730)
US-10-299-393-1
Alignment Scores:
Pred. No.: 1,118-64 Length: 2898
Score: 605.50 Matches: 109
Percent Similarity: 69.65% Conservative: 31
Best Local Similarity: 54.23% Mismatches: 44
Query Match: 57.89% Indels: 17
DB: 5 Gaps: 1
US-09-990-874B-55 (1-190) x US-10-299-393-1 (1-2898)
QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyValThr 26
DB 1437 ACTGGACGACCAACGCTACTACTCTCTGTCGACCAACGCGGAGGAGTCACT 1496
QY 27 MetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPheVal 46
DB 1497 TACACAAATGGCGACAAATGGCGAGTACAGCGTGACATGGGTGCGATTGTGCTGACTTACA 1556
QY 47 GlyGlyLysGlyTrpGlnProGly--- 54
DB 1557 TCTGGCAAGGCTGGAATCCAGCAATCCAGCAATGACAGTAACTTCTTCTTAAGCTT 1616
QY 55 -----ThrLysAsnLysValIleAsnPheSerGlySerTyrAsnProAsn 69
DB 1617 ATATTGACGTACTCACAATTTGACGAGCTGCTCAGCTACTCAGGAGCAATTTAACCCCTCT 1676
QY 70 GlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProIleGluTyrTyrIle 89
DB 1677 GGAACCGCTTATTGGCTGCTTACGCGGTGACACACAGATCTCTTGTGCAATACATCATC 1736
QY 90 ValGluAsnPheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThr 109
DB 1737 CTGGAGTCTCTCGGCGACCTATTAACCCATCATCTGACCTTACTTCTGCGGAGGTCACT 1796
QY 110 SerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGlu 129
DB 1797 AGCGATGTGGCACCTACGATATCTACTCAACCCAGCGGTGTACCCAGCTTCCATTGAG 1856
QY 130 GlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGlySer 149
DB 130 GlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGlySer 149

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Db      1857  GGAACCTTCACCTTCAACCAGTACTGGTCAGTTCCGACCGAGAAGCGAGTCGGCGGAAC 1916
QY      150  ValAsnThrAlaAsnHisphenAlaTtpAlaArgGlnGlyLeuThrLeuGlyThrMet 169
Db      1917  GTCACCCACGGCAACCACTTTGCAGCATGGAGGCACCTTGGACTTGAATGGGCACCTTAT 1976
QY      170  AspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThrVal 189
Db      1977  AACTATATGATTGTGTCCACCGAAGGCTACGAGAGCAGTGGCTCTAGTACCATCACAGTG 2036
QY      190  Ser 190
Db      2037  TCC 2039

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Search completed: December 30, 2005, 05:50:28
 Job time : 823 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2005, 03:32:53 ; Search time 895 Seconds
(without alignments)
111.289 Million cell updates/sec

Title: US-09-990-874B-55
Perfect score: 1046
Sequence: 1 QTIQGTGTHGDFYSYWN.....YQIVAVEGYFGSGSASITVS 190

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4172979 seqs, 262114271 residues

Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_p/US0990874/runat_29122005_095050_5222/app_query.fasta_1.327
-DB=Published Applications NA New -QFMT=faatap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0990874@cgn_1_1_183 @runat_29122005_095050_5222
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.*
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PTC_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 643.5 | 61.5 | 588 | 7 US-11-170-653-9 | Sequence 9, Appli |
| 2 | 497 | 47.5 | 645 | 7 US-11-170-653-10 | Sequence 10, Appl |
| 3 | 497 | 47.5 | 657 | 7 US-11-170-653-11 | Sequence 11, Appl |
| 4 | 110 | 10.5 | 774 | 6 US-10-793-626-3243 | Sequence 3243, Ap |
| 5 | 110 | 10.5 | 3007 | 6 US-10-793-626-3846 | Sequence 3846, Ap |
| 6 | 110 | 10.5 | 3090 | 6 US-10-793-626-3599 | Sequence 3599, Ap |
| 7 | 110 | 10.5 | 3864 | 6 US-10-793-626-3727 | Sequence 3727, Ap |
| 8 | 86.5 | 8.3 | 1422 | 6 US-10-509-464-2 | Sequence 2, Appli |

| | | | | | | |
|----|------|-----|--------|---|---------------------|--------------------|
| 9 | 86 | 8.2 | 273 | 6 | US-10-467-657-3589 | Sequence 3589, Ap |
| 10 | 86 | 8.2 | 273 | 6 | US-10-467-657-6439 | Sequence 6439, Ap |
| 11 | 85.5 | 8.2 | 11736 | 7 | US-11-000-463-218 | Sequence 218, App |
| 12 | 83.5 | 8.0 | 993 | 6 | US-10-467-657-237 | Sequence 237, App |
| 13 | 83.5 | 8.0 | 993 | 6 | US-10-467-657-1113 | Sequence 1113, Ap |
| 14 | 82.5 | 7.9 | 2403 | 6 | US-10-467-657-2169 | Sequence 2169, Ap |
| 15 | 82.5 | 7.9 | 2403 | 6 | US-10-467-657-6469 | Sequence 6469, Ap |
| 16 | 80.5 | 7.7 | 5682 | 7 | US-11-059-982-2 | Sequence 2, Appli |
| 17 | 80 | 7.6 | 2346 | 6 | US-10-416-047-13 | Sequence 13, Appl |
| 18 | 79 | 7.6 | 1383 | 6 | US-10-858-730-134 | Sequence 134, App |
| 19 | 78.5 | 7.5 | 179666 | 7 | US-11-121-086-67 | Sequence 67, Appl |
| 20 | 77.5 | 7.4 | 2082 | 6 | US-10-873-528-197 | Sequence 197, App |
| 21 | 77 | 7.4 | 772 | 6 | US-10-750-185-49101 | Sequence 49101, A |
| 22 | 77 | 7.4 | 1404 | 7 | US-11-000-463-663 | Sequence 663, App |
| 23 | 76.5 | 7.3 | 1422 | 6 | US-10-509-464-1 | Sequence 1, Appli |
| 24 | 76.5 | 7.3 | 1925 | 6 | US-10-909-125-815 | Sequence 815, App |
| 25 | 76 | 7.3 | 2112 | 6 | US-10-485-517-44 | Sequence 44, Appl |
| 26 | 76 | 7.3 | 70513 | 6 | US-10-995-561-13368 | Sequence 13368, A |
| 27 | 75.5 | 7.2 | 1148 | 6 | US-10-793-626-1563 | Sequence 1563, Ap |
| 28 | 75.5 | 7.2 | 3328 | 6 | US-10-793-626-4195 | Sequence 4195, Ap |
| 29 | 75.5 | 7.2 | 116856 | 7 | US-11-143-980-1 | Sequence 1, Appli |
| 30 | 75 | 7.2 | 95223 | 7 | US-11-117-187-188 | Sequence 188, App |
| 31 | 75 | 7.2 | 170189 | 7 | US-11-112-908-50 | Sequence 50, Appli |
| 32 | 74.5 | 7.1 | 3032 | 6 | US-10-533-355-3 | Sequence 3, Appli |
| 33 | 74 | 7.1 | 86081 | 6 | US-10-995-561-13246 | Sequence 13246, A |
| 34 | 73.5 | 7.0 | 711 | 6 | US-10-821-234-8 | Sequence 8, Appli |
| 35 | 73.5 | 7.0 | 1117 | 6 | US-10-821-234-222 | Sequence 222, App |
| 36 | 73 | 7.0 | 1189 | 6 | US-10-750-185-24625 | Sequence 24625, A |
| 37 | 73 | 7.0 | 3192 | 6 | US-10-131-826A-75 | Sequence 75, Appl |
| 38 | 73 | 7.0 | 65723 | 6 | US-10-995-561-13200 | Sequence 13200, A |
| 39 | 72.5 | 6.9 | 702 | 7 | US-11-173-969-9 | Sequence 9, Appli |
| 40 | 72.5 | 6.9 | 702 | 8 | US-11-173-320-9 | Sequence 9, Appli |
| 41 | 72.5 | 6.9 | 777 | 6 | US-10-513-184-6 | Sequence 6, Appli |
| 42 | 72.5 | 6.9 | 777 | 6 | US-10-513-184-8 | Sequence 8, Appli |
| 43 | 72.5 | 6.9 | 987 | 6 | US-10-512-184-57 | Sequence 57, Appl |
| 44 | 72.5 | 6.9 | 987 | 6 | US-10-512-184-59 | Sequence 59, Appl |
| 45 | 72.5 | 6.9 | 2996 | 6 | US-10-750-185-53271 | Sequence 53271, A |

ALIGNMENTS

RESULT 1
US-11-170-653-9
; Sequence 9, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibito
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanuginosus
US-11-170-653-9

Alignment Scores: 2.21e-66 Length: 588
Pred. No.: 643.50 Matches: 117
Score: 74.87% Conservative: 26

Best Local Similarity: 61.26% Mismatches: 47
Query Match: 61.52% Indels: 1
DB: 7 Gaps: 1

US-09-990-874B-55 (1-190) x US-11-170-653-9 (1-588)

QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnApp 20
DB 4 CAGACAACCCCAACTCGGAGGCTGGCAGCATGTTATTACTATTCTCTGGTGGAGTGAC 63

QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 64 GGTGGAGCCAGCCACGATACCAACCTGGAGCGGCACCTTCAGAGATCAGCTGGGA 123

QY 41 AsnSerGlyAsnPheValGlyGlyLysGlyTyrGlnProGlyThrLysAsnLysValIle 60
DB 124 GATGGCGGTAACTCTCGTGGTGAAGGCTGGAACCCCGGCTGAACGCAAGAGCCATC 183

QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLysValValTyrGlyTrpSer 80
DB 184 CACTTTGAGGGTGTATTACCAAGCCCAACGCGCAACAGCTACTTGGCGGTCTACGGTTGGACC 243

QY 81 ArgAsnProLeuIleGlyTyrTrpIleValGluAsnPheGlyThrTyrAsnProSerThr 100
DB 244 CGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACTATGATCCTTCCTCC 303

QY 101 GlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCysArgThr 120
DB 304 GGTGCTACCGATCTAGAACTGTGAGTGGCGAGGTAGCATCTATCGACTCGGCAAGACC 363

QY 121 GlnArgValAsnAlaProSerIleGlyThrAlaThrPheTyrGlnTyrTrpSerVal 140
DB 364 ACTCGGCTCAACGCACTAGCTAGCTCGAGCGCACCCCAACCTTCGACCAATCTGTCGGTC 423

QY 141 ArgArgAsnArgSerSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAla 160
DB 424 CGCCAGGCAAGCGCACCGGTACCGTCCGACGCGGCTCGCACCTTCGACGCGCTGGCT 483

QY 161 ArgGlnGlyLeuThrLeu---GlyThrMetAspTyrGlnIleValAlaValGluGlyTyr 179
DB 484 CCGCTGGTGTGAATGTCACGGTGACCACTACTACAGATCGTTGCCAGGCGGCTAC 543

QY 180 PheSerSerGlySerAlaSerIleThrValSer 190
DB 544 TTCAGCAGCGGCTATGCTCGCATCACCGTTGCT 576

RESULT 2

US-11-170-653-10
; Sequence 10, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-11-170-653-10

Alignment Scores:
Pred. No.: 5,43e-49 Length: 645
Score: 497.00 Matches: 97
Percent Similarity: 69.78% Conservative: 30
Best Local Similarity: 53.30% Mismatches: 47
Query Match: 47.51% Indels: 8
DB: 7 Gaps: 6

US-09-990-874B-55 (1-190) x US-11-170-653-10 (1-645)

QY 14 PheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGly 33
DB 100 TACTCGCAAAATGACATGATGGGCGGTATAGTAAACGCTGTCAATGGTCTGGCGGG 159

QY 34 GlnPheSerValAsnTrpSerAsnSerGlyAsnPheValGlyGlyLysGlyTrpGlnPro 53
DB 160 AATTACAGTGTAAATGGTCTAATACCGGAATTTTGTGTGTAAGGTGGACTACA 219

QY 54 GlyThrLysAsnLysValIleAsnPhe---SerGlySerTyrAsnProAsnGlyAsnSer 72
DB 220 GGTTCGCCATTTAGGACGATAACTATAATGCCGAGTTTGGGCGCCGAATGCCAATGGA 279

QY 73 TyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIleGluTyrTrpIleValGluAsn 92
DB 280 TATTTAACTTATATGTTGGACGAGATCACCTCTCATAGAATATATATGTAGTGGAATCA 339

QY 93 PheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSerAspGly 112
DB 340 TGGGTACTTATAGACCT---ACTGGACGATATAA---GGTACTGTAAAAAGTGTATGGG 393

QY 113 SerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluGly---Thr 131
DB 394 GGTACATATGACATATATACAACTACAGCTTATAACGACCTTCCATTGATGGCATCGC 453

QY 132 AlaThrPheTyrGlnTyrTrpSerValArgAsnArgAspSerSerGlySer----- 149
DB 454 ACTACTTTTACCGCACTACTGGAGTGTCCGAGTTCGAAGAGACCAACCCGGAAGCAACGCT 513

QY 150 ---ValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThr 168
DB 514 ACATACACTTTTCAGCAATCATGTGAACGATGGAAGACCATGGAATGATCTGGGCAGT 573

QY 169 ---MetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIle 187
DB 574 AATTGGGCTTACCAAGTCAATGCGCAGACAGAGATATCAAAGTAGTGAAGTCTTAACGTA 633

QY 188 ThrVal 189
DB 634 ACAGTG 639

RESULT 3

US-11-170-653-11
; Sequence 11, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 11
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: B. subtilis xylanase sequence with added restriction site
US-11-170-653-11

Alignment Scores:
Pred. No.: 5,57e-49 Length: 657
Score: 497.00 Matches: 97
Percent Similarity: 69.78% Conservative: 30
Best Local Similarity: 53.30% Mismatches: 47
Query Match: 47.51% Indels: 8
DB: 7 Gaps: 6

US-09-990-874B-55 (1-190) x US-11-170-653-11 (1-657)

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QY 14 PheTyrSerTyrTrpAsnAspGlyHisGlyGlyValThrMetThrLeuGlyProGlyGly 33
DB 106 TACTGGCAAAATGGAGTCTATGGGGCGGTATAGTAAACGCTGTCAATGGGTCTGGCGGG 165
QY 34 GlnPheSerValAsnTrpSerAsnSerGlyAsnPheValGlyGlyGlyTrpGlnPro 53
DB 166 AATTACAGTGTAAATGGTCTAATACCGGAAATTTTGTGTTGGTAAAGTTGGACTACA 225
QY 54 GlyThrLysAsnLysValIleAsnPhe---SerGlySerTyrAsnProAsnGlyAsnSer 72
DB 226 GGTTCGCCAATTAGGACGATAACTATAATGCGGAGTTTGGCGCGCGAATGGCAATGGA 285
QY 73 TyrLeuAlaValTyrGlyTrpSerArgAsnProGluIleGluTyrTyrIleValGluAsn 92
DB 286 TATTTAACTTTATATGTTGGACGAGATCACTCTCATAGATATATATGTAGTGGATTCA 345
QY 93 PheGlyThrTyrAsnProSerThrGlyAlaThrLysHisGlyGluValThrSerAspGly 112
DB 346 TGGGGTACTTATAGACCT---ACTGAAAGCTATAAA---GGTACTGTAAAGTGTATGGG 399
QY 113 SerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIleGluGly---Thr 131
DB 400 GGTACATATGACATATATACACTACACGTTTATAACGACCTTCCATTGATGCGGATCGC 459
QY 132 AlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGlySer-----149
DB 460 ACTACTTTTACGCGAGTACTGGAGTGTTCGCGAGTGGACCAACCGGAGCAACGCT 519
QY 150 ---ValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThr 168
DB 520 ACAATCACTTTCAGCAATCATGTGAACGCGATGGAAGAGCGCATGGAATGAATCTGGCAGT 579
QY 169 ---MetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIle 187
DB 580 AATTGGGCTTACCAGTCTACGCGACAGAGGATATCAAAGTAGTGAAGTTCTTAACGTA 639
QY 188 ThrVal 189
DB 640 ACAGTG 645
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RESULT 4

US-10-793-626-3243
; Sequence 3243, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793, 626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3243

; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3243

Alignment Scores:
Pred. No.: 0.00431 Length: 774
Score: 110.00 Matches: 55
Percent Similarity: 31.36% Conservative: 19
Best Local Similarity: 23.31% Mismatches: 76
Query Match: 10.52% Indels: 86
DB: 6 Gaps: 11

US-09-990-874B-55 (1-190) x US-10-793-626-3243 (1-774)

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QY 4 GlnProGlyThrGlyTyr-----HisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 85 CAAATAATATGATGGGTACAATCCAAACGACCCCTTATTTCATATAGCTAC-----132
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSerAsn 41
DB 133 -----ACTTACACATCGATCGTGAAGTAACTACCACCTACACTTGG-----174
QY 42 SerGlyAsnPheValGlyGlyGlyTrpGlnProGlyThrLysAsnLysValIleAsn 61
DB 175 AAGGTAAAC-----TGGAGTCCAGATCGGTAAATACT-----207
QY 62 PheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 208 -----TCATATACTATAATAATACTATACTACAACACTACTATGTTGTTAC-----252
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsn-----97
DB 253 AATAACTATAGCACTACATAACTACAGTAACTATTAACAACATTAACAACACTATCAATCA 312
QY 98 -----ProSerThrGlyAlaThrLysHisGlyGluVal 108
DB 313 AACACACGCAATCACAAAGAACAACTCAACGCGACTGGTGGTTTAGGGCGCAAGCTATTCA 372
QY 109 ThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIle 128
DB 373 ACATCAAGTAGTAATATGTTTAC-----GTTCAACAACACTTCTCGCGCATCATCA 420
QY 129 GluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgSerSerGly 148
DB 421 AACGGTGTA-----TCTTTATCAACGCTCGCTCAGCACTGCT 459
QY 149 SerVal-----150
DB 460 AACTTATACACTTCAGGTCAATGTACATATTATGATTGTGACAGAGTAGGTGGCAAAATC 519
QY 151 -----AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThr 165
DB 520 GGTTCACGCTGGGGTAAACGCAACAACTGGGCAACGCTGCAGCAGCTTCTGTTTACACA 579
QY 166 LeuGlyThrMetAspTyrGln-----172
DB 580 GTAAACAATTCGCTGCTTAAGGTGAATCTTACAAACGCTCAAGGTGCATACGACAC 639
QY 173 IleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThr 188
DB 640 GTAGCATCGTTGAAGGTGTAACACGCAATGTTTCAATCAGAGTTTCA 687
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RESULT 5

US-10-793-626-3846/c
; Sequence 3846, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3846
LENGTH: 3007
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence

US-10-793-626-3846

Alignment Scores:
Pred. No.: 0.0285 Length: 3007
Score: 110.00 Matches: 55
Percent Similarity: 31.36% Conservative: 19
Best Local Similarity: 23.31% Mismatches: 76
Query Match: 10.52% Indels: 86
DB: 6 Gaps: 11

US-09-990-874B-55 (1-190) x US-10-793-626-3846 (1-3007)

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QY 4 GlnProGlyThrGlyTyr-----HisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 2139 CAAAATAATGATGGGTACCAATCAACAGCCCTTATTCATATAGCTAC-----2092
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsn 41
DB 2091 -----ACTTACCAATCGATCGTGAAGGTAACCTACCACCTACTTGG-----2050
QY 42 SerGlyAsnPheValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIleAsn 61
DB 2049 AAAGGTAAC-----TGGAGTCCAGATCGTGTAAATACT-----2017
QY 62 PheSerGlySerTyrAsnProGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 2016 -----TCATATAACTATTAATAATTAATACTACCACTACTTGGTTAC-----1972
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsn-----97
DB 1971 AATACTATAGCAACTACAACTACAGTAACTACCAATTAACAACAACTATCAATCA 1912
QY 98 -----ProSerThrGlyAlaThrLysHisGlyGluVal 108
DB 1911 AACACACGCAATCACAAAGAACAACTCAACCGACTGGTGTAGGCGCAAGCTATTCA 1852
QY 109 ThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIle 128
DB 1851 ACATCAAGTAGTAATGTTTCAC-----GTTTACAACAACCTTCTCGGCATCATCA 1804
QY 129 GluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerSerGly 148
DB 1803 AACGGTGTA-----TCTTTATCAACGCTCGCTCAGCACTGTGT 1765
QY 149 SerVal-----150
DB 1764 AACTTATACACTTCAGGTCAATGTACATATTATGTTTGCACAGAGTAGGTGGCAAAATC 1705
QY 151 -----AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThr 165
DB 1704 GGTTCACCGTGGGTAAACGCAAACTCGGCAACGCTGCAGCAGCTTCTGTGTACACA 1645
QY 166 LeuGlyThrMetAspTyrGln-----172
DB 1644 GTAAACAATTCACCTGCTAAAGGTGCAATCTTACAAACGTCACAAGTGCATACGACAC 1585
QY 173 IleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleThr 188
DB 1584 GTAGCATACGTTGAAGGTGTAACACGCAATGTTTCAATCAGAGTTTCA 1537
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RESULT 6

US-10-793-626-3599/c
Sequence 3599, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3599
LENGTH: 3090
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence

US-10-793-626-3599

Alignment Scores:

Pred. No.: 0.0296 Length: 3090
Score: 110.00 Matches: 55
Percent Similarity: 31.36% Conservative: 19
Best Local Similarity: 23.31% Mismatches: 76
Query Match: 10.52% Indels: 86
DB: 6 Gaps: 11

US-09-990-874B-55 (1-190) x US-10-793-626-3599 (1-3090)

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QY 4 GlnProGlyThrGlyTyr-----HisAspGlyTyrPheTyrSerTyrTrpAsnAspGly 21
DB 2439 CAAAATAATGATGGGTACCAATCAACAGCCCTTATTCATATAGCTAC-----2392
QY 22 HisGlyGlyValThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsn 41
DB 2391 -----ACTTACCAATCGATCGTGAAGGTAACCTACCACCTACTTGG-----2350
QY 42 SerGlyAsnPheValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIleAsn 61
DB 2349 AAAGGTAAC-----TGGAGTCCAGATCGTGTAAATACT-----2317
QY 62 PheSerGlySerTyrAsnProGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArg 81
DB 2316 -----TCATATAACTATTAATAATTAATACTACCACTACTTGGTTAC-----2272
QY 82 AsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsn-----97
DB 2271 AATACTATAGCAACTACAACTACAGTAACTACCAATTAACAACAACTATCAATCA 2212
QY 98 -----ProSerThrGlyAlaThrLysHisGlyGluVal 108
DB 2211 AACACACGCAATCACAAAGAACAACTCAACCGACTGGTGTAGGCGCAAGCTATTCA 2152
QY 109 ThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaProSerIle 128
DB 2151 ACATCAAGTAGTAATGTTTCAC-----GTTTACAACAACCTTCTCGGCATCATCA 2104
QY 129 GluGlyThrAlaThrPheTyrGlnTyrTrpSerValArgAsnArgArgSerSerGly 148
DB 2103 AACGGTGTA-----TCTTTATCAACGCTCGCTCAGCACTGTGT 2065
QY 149 SerVal-----150
DB 2064 AACTTATACACTTCAGGTCAATGTACATATTATGTTTGCACAGAGTAGGTGGCAAAATC 2005
QY 151 -----AsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThr 165
DB 2004 GGTTCACCGTGGGTAAACGCAAACTCGGCAACGCTGCAGCAGCTTCTGTGTACACA 1945
```


Db 331 ATACCTGCTTGCAGATGCTTGAACCTTGGCTGCTACAGGATCATCGAAACCCACCT 390
Qy 98 ProSerThrGlyAlaThrIleGlyHisGlyGluValThrSerAspGlySerValTyrAspIle 117
Db 391 CCTTAACCTGGCACCGATAAAGCTCCAAACATCATCAAACTTGCATCATGATTTT 450
Qy 118 CysArgThrGlnArgValAsnAlaProSerIleGlu---GlyThrAlaThrPheTyr--- 135
Db 451 TGTGGAGTCAGAGTTTCAAGTTTCTGGAGTGAGTCAGGCTATGCTTCTCTGTGGA 510
Qy 136 -----GlnTyrTrp-SerValArg-----AsnArgArgSerSerG1 148
Db 511 AACAACTCTGATTACTGAAGTACGGAGGAGGAGGAGGAGTACCGAATGCAACAGCGTCTGC 570
Qy 148 ySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyTh 168
Db 571 TTCGGGATCATCACCCAAAC----- 589
Qy 168 rMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSerIleTh 188
Db 590 -----CCTGTGGTGGCGATG-----GCAGATCATCTCTTTTGC 624
Qy 188 rValSer 190
Db 625 ACTCTCG 631

RESULT 9

US-10-467-657-3589
; Sequence 3589, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3589
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3589

Alignment Scores:
Pred. No.: 0.699 Length: 273
Score: 86.00 Matches: 27
Percent Similarity: 52.05% Conservative: 11
Best Local Similarity: 36.99% Mismatches: 23
Query Match: 8.22% Indels: 12
DB: 6 Gaps: 4

US-09-990-874b-55 (1-190) x US-10-467-657-3589 (1-273)

Qy 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyVal 25
Db 61 GGTAGCGGCTATGGCAACGGCTACGGCAACGGCTACGGCAAC---GGCTACGGCGCGTC 117
Qy 26 ThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPhe 45
Db 118 -----GGCGGGCGCGGT-----AGCGGACGGC---TAC 144
Qy 46 ValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIleAsnPheSerGlySer 65
Db 145 GGCACGGCAACGGCTACAGCAACGGCGGACGGCGGACGGCGGACGGCGGCAAC 204

Qy 66 TyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGly 78
Db 205 GGTAGCGGCAACGGCTATGGCAACGGCTACGGC 243
RESULT 10
US-10-467-657-6439
; Sequence 6439, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6439
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6439

Alignment Scores:
Pred. No.: 0.699 Length: 273
Score: 86.00 Matches: 27
Percent Similarity: 52.05% Conservative: 11
Best Local Similarity: 36.99% Mismatches: 23
Query Match: 8.22% Indels: 12
DB: 6 Gaps: 4

US-09-990-874b-55 (1-190) x US-10-467-657-6439 (1-273)

Qy 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsnAspGlyHisGlyVal 25
Db 61 GGTAGCGGCTATGGCAACGGCTACGGCAACGGCTACGGCAAC---GGCTACGGCGCGTC 117
Qy 26 ThrMetThrLeuGlyProGlyGlnPheSerValAsnTrpSerAsnSerGlyAsnPhe 45
Db 118 -----GGCGGGCGCGGT-----AGCGGACGGC---TAC 144
Qy 46 ValGlyGlyLysGlyTrpGlnProGlyThrLysAsnLysValIleAsnPheSerGlySer 65
Db 145 GGCACGGCAACGGCTACAGCAACGGCGGACGGCGGACGGCGGACGGCGGCAAC 204
Qy 66 TyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGly 78
Db 205 GGTAGCGGCAACGGCTATGGCAACGGCTACGGC 243

RESULT 11

US-11-000-463-218/c
; Sequence 218, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463

```

; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 11736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (229)..(11253)
US-11-000-463-218

Alignment Scores:
Pred. No.: 150 Length: 11736
Score: 85.50 Matches: 28
Percent Similarity: 32.77% Conservative: 11
Best Local Similarity: 23.53% Mismatches: 33
Query Match: 8.17% Indels: 47
DB: 7 Gaps: 5

US-09-990-874b-55 (1-190) x US-11-000-463-218 (1-11736)
QY 6 GlyThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrp----- 18
DB 4900 GGCCTCGGCGCACCATTCAAGCACTCGGTATAGTGTGGGTCGCCATGGGCGATGTGCT 4841
QY 19 -----AsnAspGlyHisGlyGlyValThr----- 26
DB 4840 CGGCTACCAAGAGAGCTCCATGTTGCTCAGGTGGCAGAACTGGTGCAGCTCCACTGAGG 4781
QY 27 ---MetThrLeuGlyProGly-----GlyGlnPheSerValAsnTrpSer 40
DB 4780 CTTGCAGCTGTCAGGCGCGGATGCCAGATGCCCTGCAGAAAGCTCCAGCTCCGAGGT 4721
QY 41 AsnSerGlyAsnPheValGlyGlyLysGly----- 50
DB 4720 GCTTCTGGGTCTCTTCAGAGTGGCGGGAGGCGGCCATGCCATGGCCATGGAGCGGA 4661
QY 51 -----TrpGlnProGlyThrLysAsnLysValIleAsnPheSerGlySerTyr 66
DB 4660 GGCAGCCCATCTGGCAGCCAGG-----TCCGCTCTCAC 4625
QY 67 AsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrpSerArgAsnProLeuIle 85
DB 4624 TCTCCAGCTGTTGGTGGCGTCTTCTGCAGCCTCTGGCTGGAGCGCAGGTCTCGCCCTG 4568

RESULT 12
US-10-467-657-237
; Sequence 237, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

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; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 237
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-237

Alignment Scores:
Pred. No.: 832 Length: 993
Score: 83.50 Matches: 51
Percent Similarity: 33.33% Conservative: 21
Best Local Similarity: 23.61% Mismatches: 71
Query Match: 7.98% Indels: 73
DB: 6 Gaps: 12

US-09-990-874b-55 (1-190) x US-10-467-657-237 (1-993)
QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTrpAsn-----App 20
DB 265 TCATCTAGCGCGACCCCATAAACCGTCAGCTACTCTCCCGCATTTCAAAATTCGCGAC 324
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 325 CGCAGCAGCAGG-----CAGCGCTCGCGACGCGCGCATCTTTATCTGTGCGACG 378
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlnProGlyThrLysAsnLysValIle 60
DB 379 GACTCC-----GGGGTACTCTCGTATGCGGAAATTAACCAACAGATTATATG 426
QY 61 AsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAlaValTyrGlyTrp 79
DB 427 AAATTCGGGGCGTGGATAGTCTTAACGCGGAAATCGACCTCTTCGCGCGCGCTTCCCC 486
QY 80 ---SerAsnProLeuIleGluTyrTrpIleValGluAsnPheGlyThrTyrAsnPro 98
DB 487 GTCGCGCAAAACCGCGCTCTCGCTTC-----TCTACGCGCAGCAGCAGCGCC 534
QY 99 SerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCys 118
DB 535 GAAACCGCATTTGCTCAAG---GGTAAATCACT----- 564
QY 119 ArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrp 138
DB 565 -----TATCAGGTTTGG 576
QY 139 SerValArg---ArgAsnArgArg-----SerSerGly 148
DB 577 GGCATCCGCGTCCAGAAACGCGCAATTTGTACTTCTTATACGCCCGCGCGCGT 636
QY 149 SerValAsn-----ThrAlaAsnHisPhe 156
DB 637 TCTTATATGGACACTTCCCAATACCCCGCTCTTTCTTTATACCCCGCAAT---TTC 693
QY 157 AsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyr----- 171
DB 694 AACAGCAACACACTGGCAGGCAAAATCTTCGCGACAGCGATTACGGCGCGGATGGAT 753
QY 172 ---GlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
DB 754 ATTCAAAACGCAACGATTACCGTCCGACCTTTTCGGCGGATGCCACG 801

RESULT 13
US-10-467-657-1113
; Sequence 1113, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; CURRENT APPLICATION NUMBER: US/10/467,657

```

; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1113
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1113

Alignment Scores:
Pred. No.: 8.32 Length: 993
Score: 83.50 Matches: 51
Percent Similarity: 33.33% Conservative: 21
Best Local Similarity: 23.61% Mismatches: 71
Query Match: 7.98% Indels: 73
DB: 6 Gaps: 12

US-09-990-874B-55 (1-190) x US-10-467-657-1113 (1-993)

```
QY 7 ThrGlyTyrHisAspGlyTyrPheTyrSerTyrTyrAsn-----Aap 20
DB 265 TCATCTACGCGACGCCCAATACCGTCAGCTACTCTCCCGGATTCAAAATTCCCGAC 324
QY 21 GlyHisGlyGlyValThrMetThrLeuGlyProGlyGlyGlnPheSerValAsnTrpSer 40
DB 325 CCACAGCAGGG-----CAGCGGCTCGCGAGCGCGCGCATCTTTATCTGTCGACG 378
QY 41 AsnSerGlyAsnPheValGlyGlyGlyGlyTyrGlnProGlyThrLysAsnLysValle 60
DB 379 GACTCC-----GGGGCTACTTCGTATGCGGAAATTACCAAAACAAGATTATATG 426
QY 61 AsnPheSerGlySerTyrAsnProGlyGlyGlnPheSerTyrLeuAlaValTyrGlyTrp 79
DB 427 AAATTTCGGGGCGTGATAGTCTTACGCGGAAATCGACCTCTTCGCGGCGGCTTCCCC 486
QY 80 ---SerArgAsnProLeuIleGluTyrTyrIleValGluAsnPheGlyThrTyrAsnPro 98
DB 487 GTCGCAAAACCGCGCTCTCTCGGTC-----TCCTACGCGACGACGCGCC 534
QY 99 SerThrGlyAlaThrLysHisGlyGluValThrSerAspGlySerValTyrAspIleCys 118
DB 535 GAAACCGCATTTCTCAAG--GTTAAATCACT----- 564
QY 119 ArgThrGlnArgValAsnAlaProSerIleGluGlyThrAlaThrPheTyrGlnTyrTrp 138
DB 565 -----TATCAGGTTGG 576
QY 139 SerValArg---ArgAsnArgArg-----SerSerGly 148
DB 577 GCATCCGGCTCAGAAACCGGCAATTTGTACTTCTCTTATACGCGCGCAAAAGCGT 636
QY 149 SerValAsn-----ThrAlaAsnHisPhe 156
DB 637 TCTTATTGGGACACTTGCCAATACCCCGCTCTTCTTTATCACCGCCAAT---TTC 693
QY 157 AsnAlaTrpAlaArgGlnGlyLeuThrLeuGlyThrMetAspTyr----- 171
DB 694 AACAGCAACACACTGCGCAGGCAAAATCTTCGGCAACACAGCGATTTACGGGCGCGATGTGGAT 753
QY 172 ---GlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSer 186
DB 754 ATTCAAAACCGCAACGATTACCGGTCGACCTTTTCGGCGATGCCACG 801
```

RESULT 14

US-10-467-657-2169/c

; Sequence 2169, Application US/10467657

; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2169
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2169

Alignment Scores:
Pred. No.: 37.4 Length: 2403
Score: 82.50 Matches: 52
Percent Similarity: 34.29% Conservative: 32
Best Local Similarity: 21.22% Mismatches: 97
Query Match: 7.89% Indels: 64
DB: 6 Gaps: 9

US-09-990-874B-55 (1-190) x US-10-467-657-2169 (1-2403)

```
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAsp----- 11
DB 1197 CAGACGCTGGCAACCAAGCGGCTACAAAGACGAACCTTAGCCCATCATGCCGCCCTT 1138
QY 12 -----GlyTyrPheTyr 15
DB 1137 TCTGCCGATTGGCATAAACGCGAGCGGCGCAAAATCGGGGTGTCCGCACAAATTTACC 1078
QY 16 SerTyrTrpAsnAspGly---HisGlyGlyValThrMetThrLeuGlyProGlyGln 34
DB 1077 CGCTTCAGCCAGCGCGCGCGGCGGCAAGACGCGACCGACCTGCTGTATCCCGGT----- 1024
QY 35 PheSerValAsnTrp-----SerAsnSerGlyAsnPheVal----- 46
DB 1023 -----ATCAATGGGATTTTCAGCAACAGCTCGGGCTACGTCGCGCCCAACTCGGGCTG 970
QY 47 -----GlyGlyLysGlyTyrGlnPro---GlyThr 55
DB 969 CACGCCACTTATTACAGCTCGACAGTTTCGGCGGCAAAAGCATCCCGCAGCGCTCGGGCGC 910
QY 56 LysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAla 75
DB 909 GTTTTGGCGCGGTGTCAATATATCGACGCGCGCAACACTTCGAACGCAATACGCGCTG--- 853
QY 76 ValTyrGlyTrpSerArgAsnProLeuIleGluTyrTyrIleValGluAsnPhe----- 93
DB 852 ---TTCGCGCGGAGTGTGTCNAACCATCGCAACCATCGAGCGCGCTGTTCTACATATATTCCT 796
QY 94 -----GlyThrTyrAsnProSerThrGlyAlaThrLysHisGly 106
DB 795 GCCAAATCTCAAAACGACCTGCCCAATTTTCGTCGCGGAAAGCAGCTTCGGCTACGGG 736
QY 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
DB 735 CAGCTTTTCGCGAAACCTCTATTACGGC-----AACGACCGCATCAACGCCGCC 685
QY 127 SerIleGluGlyThrAlaThrPheTyrGln-TyrTrpSerValArgAsnArgArgSe 146
DB 684 AACAGCCTTTCACCGCGCTGCAGAGCGGTATTTGGACGGCGCGCGCGGAGGAGCGT 625
QY 146 rSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrle 166
```

Db 624 TTCGCGCGGTATCGGTGAGAAATCTATTTCAAGGATGATCGGTGATGCTTGACGGC 565
QY 166 uGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSe 186
Db 564 ACCTGCGGCAAAATCCGGCGAGCGCTTCGAGCTGGGTGGCATTCGCTCCGGCGGCATA 505
QY 186 rIleThrValSer 190
Db 504 GCGGCGCGTTTCA 492

RESULT 15
US-10-467-657-6469
; Sequence 6469, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6469
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6469

Alignment Scores:
Pred. No.: 37.4 Length: 2403
Score: 82.50 Matches: 52
Percent Similarity: 34.29% Conservative: 32
Best Local Similarity: 21.22% Mismatches: 97
Query Match: 7.89% Indels: 64
DB: 6 Gaps: 9

US-09-990-874b-55 (1-190) x US-10-467-657-6469 (1-2403)
QY 1 GlnThrIleGlnProGlyThrGlyTyrHisAsp----- 11
Db 1207 CAGACGCTGGCAACCAAGCGGCTACAAAGACAACTTACGCCATCATGCCCGCCCTT 1266
QY 12 -----GlyTyrPheTyr 15
Db 1267 TCTGCGGATGGCATAAACGAGCGGCGGCAATCGGCGTGTCGCGACAAATTTACC 1326
QY 16 SerTyrTrpAsnAspGly---HisGlyGlyValThrMetThrLeuGlyProGlyGlyGln 34
Db 1327 CGCTTCAGCCACGACGCGGCCCAAGAGCGGCGAGCGGCTGCTGTATCCCGGT----- 1380
QY 35 PheSerValAsnTrp-----SerAsnSerGlyAsnPheVal----- 46
Db 1381 -----ATCAATGGGATTTACGACACAGCTGGGGCTACGTCGCGCCCAACTCGGGGTG 1434
QY 47 -----GlyGlyLysGlyTyrGlnPro-----GlyThr 55
Db 1435 CAGGCCACTTATTACAGCTCGACAGTTTCGGCGGCAAGCATCCCGCAGCGTCCGGCGC 1494
QY 56 LysAsnLysValIleAsnPheSerGlySerTyrAsnProAsnGlyAsnSerTyrLeuAla 75
Db 1495 GTTTTCGCCGTGTCAATATCGAGCGGCGGCAACCTTCGAACGCAATACGCGCTG--- 1551
QY 76 ValTyrGlyTrpSerArgAsnProLeuIleGlyTyrIleValGluAsnPhe----- 93
Db 1552 ---TTCGGCGGCGAGTTCGTGCAAAACCATCGAGCGCGCTGTCTACAACTATATTCCT 1608
QY 94 -----GlyThrTyrAsnProSerThrGlyAlaThrLysHisGly 106

Db 1609 GCCAAATCTCAAAACGACCTGCCCAATTCGATTTCGGAAGCAGCTTCGGCTACGGG 1668
QY 107 GluValThrSerAspGlySerValTyrAspIleCysArgThrGlnArgValAsnAlaPro 126
Db 1669 CAGCTTTTCCGCGAAGAACTCTATTACGGC-----NACGACCGCATCAACGCGCC 1719
QY 127 SerIleGluGlyThrAlaThrPheTyrGln-TyrTrpSerValArgAsnArgArgSe 146
Db 1720 AACAGCCTTTCACCGCGGTGCAGAGCGGTATTTGGACGCGCGGACGGGGAGAGCGT 1779
QY 146 rSerGlySerValAsnThrAlaAsnHisPheAsnAlaTrpAlaArgGlnGlyLeuThrIe 166
Db 1780 TTCCCGCGGATTCGGTCAGAAATCTATTTCAGGATGATCGGTGATGCTTGACGGC 1839
QY 166 uGlyThrMetAspTyrGlnIleValAlaValGluGlyTyrPheSerSerGlySerAlaSe 186
Db 1840 AGCGTCGGCAAAATCCCGCAGCGCTTCGAGCTGGGTGGCATTCGCTCCGGCGGCATA 1899
QY 186 rIleThrValSer 190
Db 1900 GCGGCGCGTTTCA 1912

Search completed: December 30, 2005, 06:05:33
Job time : 902 secs